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108884 Sequence 2
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AL731825 Bacillus th
201676 DNA sequence 1
108093 Sequence 1
108103 Sequence 1
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201038 Sequence 3
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Bacillus thuringiensis
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5980; Conservative 0; Mismatches 0; Indels 0;
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AB07413 Bacillus
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Listing first 45 summaries
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                                                                         GIGTCAGCACTITCTATATGTGATITATTATCTATAATTCGTAAAGAGGTAGCCGATAGT
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/ codon start=1
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/ product="putative mosquitocidal toxin"
/ db_xref="qs:31745044"
/ franslation="wwsYowkwexeilkrebagesyndoning spwnbowsstatcolic strkevDesvisharefordynyroffyrfareforestry strkevDesvishareforestry mosquitocidal toxing sets premiure putative mosquitocidal toxing sets premiure putative mosquitocidal toxing sets premiure mosquitocidal toxing toxing
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/ codon start=1 |
/ codon start=1 |
/ broducT = "hypothetical protein" |
/ producT = "hypothetical protein" |
/ producT = "hypothetical protein" |
/ producT = "id = "BAC77649.1" |
/ db xref = "id : 174549." |
/ db xref = "id : 174
                                                                                                                                                                                  ito,T., Sahara,K., Asano,S. and Bando,H.
Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringienesis subsp. aizawai Encoding Mosquitocidal Proteins
Unpublished
(bases 1 to 4100)
Ito,T., Sahara,K., Asano,S. and Bando,H.
Direct Submission
Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience; Kita-9jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail:ito-t@abb.agr.hokudai.ac.jp, Tel:81-11-706-2487(ex.2487))
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GNCOLAMRRNRGGGVYQEAAHTVQRTFSGSWTYDSFKYLDIFTMPAEDYTFDLTIDL
ESGGALYIDKIEFIPDDLTTLEYEEBRNLEKTRNANNDLFTN"
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/mol_type="genomic DNA"
/strain="Bun1-14"
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Pred. No. 0;
); Mismatches 716; Indels
                              Bacillus thuringiensis serovar aizawai
Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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/note="putative"
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SAENVRSELISPNSGODFTGYYERLKCKTARYTNYCLYWYQVGLNQIKGGGTGADTW

SKENKFRREMTLAVLDIIAIFPTYDPEKYPLPTHVELTRRIYTDAVGYSSGTYSWLRN
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3453 TACAGGGATGGCACGCAGCCGGAAAGGCAGCGGTACAACAGATCGATGGCGCTTCTGTAT 3512
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Bacillus thuringiensis
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                                                                                                                    GATATATGTTACGTGTGATTGCTAAAAAAGAAGGACCTGGAAAAGGAAAGGACGTGGATGTAGTAA
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Athenix Corporation (US)
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Bacillus thuringiensis serovar aizawai cry39A and 39orf2 genes for mosquitocidal toxin and Cry39ORF2 protein, partial and complete
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Bacillus thuringiensis serovar aizawai
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KRWETQQAYDPRACAVDALFTNRGELHYHITLDHIQNADRLVQSIPYYYHNULDNAPG
MYYDYYQELLNARIMQGYNLYDARNVITNGDFTQGLQGWHATGNAAVQMDGASVLVLS
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/ product = "mosquitocidal toxin" |

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TPSGCOBRCESSSRYVSGGYFTPYTDGYASGRYACGGROFGTHYTHVGNEKKWRGHMEK
KRWETQQAYDPAKQAVDAFTNEQELHYHITLDHIQNADRLAGATANQCQMDGAPG
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NWSAGVSQULHVQEHGYMLRVIAKKEGFGKGYVTWMDCNGNRETLKFTSCEGTWTK
TVBFFPESDRYRIEIGBTFFFYDSIELLCMQGYABNNNPHTGNWYGQSYNGNYNQN
TSDVYHQGYTNNYNQNSSNWYNQNYTHNDDLHSGCTCNQGHNSGCTCSQG"
Cloning and Expression of Novel Crystal Protein Genes cry39A and 390xf2 from Bacillus thuringiensis subsp. aizawai Bunl-14 Encoding Mosquitocidal Proteins

Mosquitocidal Proteins

Insect Blotechnol. Sericology 71, 123-128 (2002)

Insect Submission

Direct Submission

Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Applied Bioscience; Kita 9-jyo, Nishi 9-choume, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (B-mail:to-teabs.agr.hokudai.ac.jp, Tel:81-011-706-2487,
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                                                                                                                                                                                                                                                                                                                                           organism="Bacillus thuringiensis serovar aizawai"
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Location/Qualifiers
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                                               CTATGTTTATCAGTAATATAAAAAATACGCTAAAAATAGAAACGACAGATTATGAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                   ATAATTTACTAGAATAGGTGGTATTGCTGTTTAACAAATAAGCGAAAAAGGTTGTGAGTC
                                                                                                                                                                                                                                                                                                                                                          ATGGAGACTTTTCTG-----GGAATGATTGGACATTCGGTAATGATATTATCATAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGAAAGCATGTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTGACACCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2649 GTACAAAGCATGTGACACGATCGTCATCCATTTGATTTTCATATTGACACCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAGGACCACTAACAGGTGAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2829 TAACGCATGTGAAACAAAAGGAAAAGAAATGGAAAACAACACATGGAGAAAAACGTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATGTTTACAAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAATAATCCTATTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACTCTATTTCCAACCTATATCTGTCAAAAATAGATGAGTCTAAAATTAAAACCATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCTACACC----AACAGATGGATATGCTCCCGATATGTATGCATGCCCGCAAAATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTAGATACAAATACAAACGTAGTATTGATGTCTTATTTAAAATTTCTAATCCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2240 GGATGAAGTAAAACATGCAAAACAGCTCAGTCAGTCTCGTAATTTACTCCCAAAATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2143 TCGACAAAATTGAATTCCTCCCAAGTAATACAACAACTTTAGAATATGAGGGAGAACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1946 TAGATAGAATTGAATTTCTTCCAATAACTCAATCTGTATTAGATTATACAGAGGAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2006 ACATAGAAAAATCACAGAAAGCGGTGAATGACCTCTTTATCAATTAAAACAAA----GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAAGTGGTACGAAAAAAGATGTAAAAATTAGAAACGACAGATTATGAAATAGAATCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGAAATAAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTAGAAAAAACAAAGAACGCGGTGAACGATCTGTTTACCAATTAAAACAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTAGAATAGGTGGTATTGCTGTTTAACAAATAAGCGAAAAAGGTTGTGAGTCCTATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%; Score 1038.8; DB 1; Length 3752; 76.3%; Pred. No. 1.2e-161; Live 0; Mismatches 397; Indels 27;
                                                                                                serovar="entomocidus"
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1. .2052
                                                                                                                                                                                /gene="cry30Aa like"
                                                                                                                                                                                                                                      gene="cry30Aa like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.4
Best Local Similarity 76.3
Matches 1364, Conservative
                                                                                                                                                                                                          .2052
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Direct Submission
Submitted (124-027-2003) Tomonori Ikeya, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience;
Kitae-jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
(E-mail:ikeyan@abs.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB125059 3752 bp DNA linear BCT 28-OCT-2003
Bacillus thuringiensis serovar entomocidus cry30Aa like gene for
putative mosquitocidal toxin and hypothetical protein gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asano,S.
s from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTATAATGGAAATTATAATCAAAATACTAGCGATGTGTATTACCAAGGGTATACAAACA 3866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTATAACCAAGACTCTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGC 3926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCCGGTTGCACATGTAACCAAGGGCATAACTCTGGCTGTACATGTAATCAAGGATA 3984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis serovar entomocidus
Bacillus thuringiensis serovar entomocidus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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                                                                                                                                                                                                                                                                                                                                                  AAAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAGAAG
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THAKYLLSQSRNLLQWODFEDLFSGAFTSNHMSIQADONSTEKGNYLMMSGARDIYGTI
FPTYIYQKIDBSKLEWPRYLLWRGFVGSSKDLELVWRYGKEIDTIMNVPNDIPYVPS
MPVCNELYDGEQQPYSKGNVGYYNSMPVSAPSYTSDACQCMPGKRQVVCHDBHQFKFH
TOTGSVDYYNTKLGIWULFKISSPDGYATLDNLLDYBEGPWGRALAVYCKEKKWNQO
MEKKRNETKQAYDRAKQAVDALFTGEELHYNYTLSQIKNANQLVQSIPYVHNBMLPDV
PGMNYDLYQELGYYLLXARAKQAVDALFTGEELHYNYTLSQIKNANQLVQSIPYVHNBMLPDV
DLSNWSGYQSQIKJHVQHACGYVLLXVSAKCKGPGKGYYTWMGCNGKQETLIFTSCDGGYM
TKTVPPPERSRNYR EIGETEGSFYIESIELICMNGYTSNNSQNMSNWYDGSYSGNYS
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                                                                                                                                                                                                                                                         Length 3931;
                                                                                                                                                                                                                                                         Query Match
16.2%; Score 966.2; DB 1; Length
Best Local Similarity 75.9%; Pred. No. 1.1e-149;
Matches 1284; Conservative 0; Mismatches 373; Indels
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Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2
genes for putative mosquitocidal toxin and hypothetical protein,
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Cloning and Expression of Novel Crystal Protein Genes from Bacillus
thuringiensis subsp. entomocidus INA288
                                                                                                      4305
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Direct Submission
Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience;
Kita-5jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
(E-mail:ikeyan@abs.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
Fax:81-011-706-2487)
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Bioscience;
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Bacillus thuringiensis serovar entomocidus
Bacteria, Firmicutes; Bacillales; Bacillusceae; Bacillus
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Tomonori, I., Kumiko, Y., Takeshi, I., Ken, S., Shin-ichiro, A.
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FPTYIYQKIDSSKLKFYTRYLYRGFVOSSKDLELVMHYGKEIDTVWNYDNIPYVPS
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KYTVEVPPESDRVRIEGGETEGSFYIESIELCMNGYTSNNNONMSNNYDQGYINNYN
QNYTNTYEQHAVCTCNQNYNNGGCTCKQG"
                                                                                                           Objects 1 to 3668)
Objects Saltch, H., Wasano, N. and Obba, M.
Object Submission, H., Wasano, N. and Obba, M.
Submitted (16-Ju-2004) Akira Objushi, Kyushu University, Graduate School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka, Pukuoka 812-8581, Japan (E-mail:obgushi@brs.kyushu-u.ac.jp,
Tel:81-92-642-3028, Fax:81-92-642-3028)
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Sacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus
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                                              Obgushi, A., Saitoh, H., Wasano, N. and Ohba, M. Cloning and characterization of novel cry genes from a mosquitocidal Bacillus thuringiensis serovar sotto strain
                                             Ohba, M.
1 cry genes from
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                              ACCACTAACAGGTGAAGCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACA
                                                                                               CATGGAGAAAAAACGTTGGGAAACACAACAAGCCTATGATCCAGCAAAAACAGGCTGTAGA
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                                                                                                                                                             TGCATTATTTACAAATGAACAAGAGTTACACTATCATATTACTTTAGATCATATTCAAAA
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Bacillus thuringiensis cry24-like, orf2s1 genes for delta-endotoxin, hypothetical protein, complete cds. AB185105.1 GI:50539654
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KRYRNRATAVAVTNDFSSVRDQIIRLKDRFLINPENKPRELILLYAQTANFDLILYQRG

ALYADBERBDINGSISPLGSKDYYISLAAKIKETYNYCAFYRRASIALLKWRNISISW

GTYNKYRREVTLGALDLAALPRYDICTYPIQTKTELTRKYYMPSFGLQGSNYFQSLE

GLENALTHPPSLFTWLINLINLYTIRENFNPALLVSSLSGLQAISRYTQNPNRISNPAQ

GVRNGTPTQIGLNNLFVYKLSLSQYHHPNECXSIAGISDMTFYKSDYNGNAPTTQTYQ
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Cry30-like, hypothetical protein,
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Obgushi, A., Waesno, N., Saitoh, H. and Ohba, M.
Direct Submission
Submitted (26-007-2004) Akira Ohgushi, Kyushu University, Grac Submitted (26-007-2004) Akira Ohgushi, Kyushu University, Grac School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka, 812-8581, Japan (8-mail:ohgushi@brs.kyushu-u.ac.jp, Tel:81-92-642-3028)
Location/Qualifiers
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
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Pred. No. 2.4e-137;
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1 (bases 1 to 127923)

1 (bases 1 to 70 Neil, S., Ben-Dov, E., Jones, A.F., Murphy, L., Quail, M.A., Borry, C., O'Neil, S., Ben-Dov, E., Jones, A.F., Murphy, L., Quail, M.A., Complete sequence and organization of patchill, J.

Complete sequence and organization of patchill, J.

Appl. Environ. Microbiol. 68 (10), 5082-5095 (2002)
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Bacillus thuringiensis subsp. israelensis plasmid pBtoxis.
AL731825
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                                                                                                                                                                     TTACAAGGGTGGCATGCGGAAGGAAAGTAGAAGTACAGCAATTGAATGGAACGACTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGATATCTGTTACGTGTGTGCGAAAAAGAGGGGTCTGGAAAAGGCTATGTAACGTTG
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TR:Q9X319 (EMBL:AF065404) (227 aa) fasta scores: E():
8.9e-44, 78.48% id in 158 aa"
                                                                                                  Submitted (19-APR-2002) Submitted on behalf of the pBtoxis sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGGTACATTTTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATA 3762
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/protein_id="CAD30064.1"
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/gene="pBt001"
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/transl_table=
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Parkhill,J.
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FAVĖVTEESYYRNYLKYQEETLFRKYAYDQGVNLHAYIALBIEMREKLKVRGHKERTI
PSDVREWFIEAIDKLPQEKLRVIELPKQFNLLEFMRTFERLVRAGVTITAPDQVLHAM
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                                                                                                                                                                                                                                                                                                     /note="Similar to Bacillus anthracis pxo1-14 TR:Q9X2YS (EMBL:AF065404) (564 aa) fasta scores: E(): 1.6e-191,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 AGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="integrase/recombinase family protein"
/brotein id="CAD30067.1"
/brotein id="CAD30067.1"
/db xref="CA1686XX3"
/db xref="CA02.086XX3"
/db xref="CA02.086XX3"
/db xref="InterPro:IPR004107"
/db xref="InterPro:IPR004107"
/db xref="UniProt/TrEMBL:Q8KXX3"
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| Da xref="G1:216854151",
| Da xref="UniProt/TremB1.08KNX2"
| Cranslation="MAVLKDSNYIEMNTYNBIGFFKGIFWGLIFVVPFWSIMIATFIW
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yy TMHMM2.0"
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TLKRSLLKOOBGGWKHFGGMYRPLHKKYPHQIRAVIEELTTALDCTGNPLFKICKM
KGVGHTKRYTLYLSIHSDFLCSKEAGEBQHRDPFTPKATYARKAKFIEAVLQEMNIG
ELSADWNKFHVLKYTCHRQIRSVIRGLRDWVDRKGGYPTKIVYLKKLLHGTSGVQI
LDTAAKEGIYPLIAQHIPKERNSDREQAVFNEGHYSWYSLHNIKRMFKNVHALLKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="%imilar to Bacillus anthracis pxo1-17 TR:09X2Y8
[EMBL:AF065404] (47 aa) fasta scores: E(): 2.1e-12, 68.08$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="HMMPfam hit to PF02899, Phage integrase, N-terminal
                                                                               /note="Similar to N-terminus of Bacillus anthracis pxol-1
TR:Q9X2Y9 (EMBL:AF065404) (315 aa) fasta scores: E():
4.2e-56, 84.15* id in 183 aa, and to Bacillus halodurans
Bh2364 protein TR:Q9XAC5 (BBE:AP001515) (378 aa) fasta
scores: E(): 1.6e-18, 35.45* id in 189 aa, and weakly to
Lactobacillus delbrueckii integrase/recombinase orf?
                                                                                                                                                                                                                                                                                    TR:048538 (EMBL:250864) (333 ad) fasta scores: E(): 6.3, 28.88 id in 90 aa, and to Bacillus thuringiensis resolvase tnpI SW:TNRI BACTU (P10020) (284 aa) fasta scores: E(): 8.5, 23.88* id in 180 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product = "putative integral membrane protein"
                           complement (4634. .5275)
/gene="pBt005"
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complement (5364. .5507)
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complement (6451. .8160)
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199 THITACHATHAGGGARGOAGTHCAMINADAMGGACAANTGCTCCCATTTTTGGGCGATCCCCCT 1712 THITACHATHAGGGARGOAGTHCAMACAANTGCACCAANTGCGCGCTAMACAANTGCGCCCTAMACAANTGCGCCCCTAMACAANTGCGCCCCTAMACAANTGCGCCCCTAMACCAANATCACCCTAMACCAANATCACCCTAACAACAATTTATTCCTAACTTATA 100 ATTTCCTAACAAAACCCAANATCACCTCGCGCTAACCCAAATTTATATCCTAACTTATA 100 ATTTCCTAACAAAACCCAAAAATTTATATCCTAACTTATA 100 ATTTCCTAACAAAACCCAAAAATTATATCCTAACAATTTATATCCTAACTTATA 100 ATTTCCTAACAAAAACCCAAAAATTATATCCTAACAATTTATATCCAACTTATA 100 ATTTCCTAAAAAAACCCAAAAATTATATCCTAAAAATTTATACAAATTATATA 100 ATTTCCTAAAAAAAAAACCCCAAAAATTATATCCTAAAAATTATATATATATATATATATATATATATATATAT	1574 TATTIGGTIGGACACIACAACAACAACAACAACAACAACAACAATATATCCAGATAAATTA 1633 1711 CACAAATACGGGGGGGGGAGAATATACCTCAAAATACGAATATATCTGCTAAACCTT 1770 1634 CGCAAATACCTGCAGTAAAAGCTTTTGCCCTACCAGGAGATATGCAGGAGGTT 1693 1771 ATGTAATAAAAGCCT 1787 1694 ACGTCACAGGCCCT 1710
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                                                                                                                     TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTGGTTTCACGCTA
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                               AGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTT
                                                                     AGCCGCAAATCTTGTGGAATGTATTTCTGAAGAATTATATCCAAAAGAAAAAATGCTGTT
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AVYFSNL VGYFLLLLPIYAQVANFULLIRDGLINAQEWSLACAGDQLYNTWQYTKE
YIAHSITWYNKGLDVLRNKSNGQMITFPNDYKREMTIQVLDILLELESYDPRELPADKI
DNTKLSKTEFTREIYTALVESPSKSIAALEAALTRDVHLFTWLKRYFYTTTTQVDL
RFLSANKIGFEYTNESAMQESGIYGSGGGGSNLTHQTQLNSNYYKTSITDTSSBSURV
YKDDFYKIGGTLASYNSONITFPPEGLRTTFFGFSTNENTPNOPTVUNYTHILSYIKTD
VIDYNSNRVSFAWTHKIVDPNNQIYTDAITQVPAVKSNPLNATAKVIKGPGGDLV
ALTSNGTGGRAFBIQCKTSIFNDFTRSYGLRIKYANSPIVLNAYSTLGGDLV
ALTSNGTGGRAFBIQCKTSIFNDFTRSYGLRIKYANSPIVLNAYTLGFDDPIFK
GHYLHMGGARDIDGTIFFTYTOFGERSKRYNALFTNDAMDALNIGTTDVDIDQAANLVEC
ISEELYFKERWLLLDEVKNAKQLSGSRNVLQNGDFESATLGATTSDNITIGEDDPIFK
GHYLHMGGARDIDGTIFFTYIFOGGSRNCETSAVPANIGHTSDNITYGDDDAANLVCC
ISEELYFKERWLLLDEVKNAKQLSGSRNVLQNGDFESATLGATTSDNITIGEDDPIFK
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DSHQFSFTIDTGALDTNENIGVWWFKISSPDGYASLDNLEVITEGGPIDGEALSRVKH
MEKKNNDOMBAKSETQQAYDVARQARILYTTNIIRNGGYTTLANDCEBNQEK
LTFTSCEBGYITKTVDVFPDTDRVRIEIGETEGSFYIBSIELCMNE"
                                             BACISRH3

4186 bp DNA linear BCT 17-FEB-1998
Bacillus thuringiensis israelensis plaemid gene for 130 kDa
insecticidal protein (ISRH3), complete cds.
D00247

130 kDa insecticidal protein (ISRH3).
Bacillus thuringiensis serovar israelensis
Bacillus thuringiensis serovar israelensis
Bacillus thuringiensis serovar israelensis
Bacillus thuringiensis serovar israelensis
                                                                                                                                                                                                                                                                                                                                                                         protein genes of Bacillus thuringiensis var. israelensis Agric. Biol. Chem. 52, 873-878 (1988)
The genes of ISRH3 and ISRH4 that were 130 kDa insecticidalu proteins of BII were sequenced and compared with other insecticidal protein genes. ISRH3 and ISRH4 were identical in a region of the C-terminal 467 amino acids.
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    (bases 1 to 4186)
    Sen, K., Honda, G., Koyama, N., Nishida, M., Neki, A., Sakai, H.,
    Himeno, M. and Komano, T.

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.larity 67.5%; Pred. No. 1.1e-120;
Conservative 0; Mismatches 539;
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/note="Shine-Dalgarno sequence"
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/db_xref="taxon:1430"
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/note="ClaI site"
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/organism="Bacillus
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RESULT 15
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3448 ACAACAATGGATGGACTTCAGTAITAGTTCTATCAAATTGGAGGGGGGGGTATCTCA 3507
               3508 AAACTIGCAIGCICAAGAICAICAIGGAIAIGIGIIAACGIGIGAGAIIGCCAAAAAAAGAAG 3567
                                                          3613 AAATGTCCATCTCCAACATAATCATGGGTATGTCTTACGTGTTATTGCCAAAAAAGGAGG 3672
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                                                                                                                                     3628 CACTICITGCGAAGAAAAAATATATGACAAAAACAGTAGGAGGTATTCCCAGAAAGTGATCG 3687
                                                                                                                                                                                                                              3868 CTATAACCAAGACTCTAG----TAATATGTATAATCAAAATTATACTAACAATGATGA 3921
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Search completed: December 19, 2005, 21:57:00 Job time : 19559.3 secs

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ALO65514 Drosophil AGO55414 Drosophil Drosophil BH401326 AG-ND-155 AG279085 Mus muscu BH877429 hydrsup AG279085 Mus muscu CG403581 ZWMBBD024 ALO69706 Drosophil AG328748 AD288748 AD588748 ACC239945 ALL 1140 AG321 Drosophil CZ239945 ALL 1140 AG3921 Drosophil AG3997 Danio rer ALO63921 Drosophil AG3997 Danio rer ALO63921 Drosophil AG31997715 AUG3715 AU
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/db_xref="taxon:1359"
/clone lib="WG1363 Random Sequence Tag Library"
/note="Vector: pSGWUZ; Site 1: Smal; Library of
chromesomal fragments of L. Lactis strain MG1363
prepared by partial AluI digestion or by sonicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria, Pirmicutes; Lactobacillales; Streptococcaceae;
Lactococcus

( bases 1 to 2711)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
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Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: Gorchin@jouy.inra.fr
best homologue in strain IL1403 is p1346
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High quality sequence start: 30
High quality sequence stop: 2683.
Location/Qualifiers
  CZ935267
CNS000D1
AQ946120
BH401326
AG279085
BH873429
AG346348
CG403581
CNS00EVL
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CG607338
CG60738
CZ239945
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AD940248
AD940248
CG807109
BX139987
CNS0039G
AU037715
BP508716
CNO037715
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CG807081 111807E2
CG937914 MBEH073TR
CG907081 111807E2
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CG807085 1118080G0
CG807132 1118080G0
CG80713 CG80715
CG80715 11180811
CG80716 114081
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Copyright (c) 1993 - 2005 Compugen Ltd.
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- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-and sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
units. For more information on RescueMu, go to the web state 'www zmdb.iastate.edu' and follow the linke for 'RescueMu' 'Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and Ball, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail ; segref@genoscope.cns.fr
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Best Local Similarity 52.1%; Pred. No. 4.3e-06;
Matches 173; Conservative 0; Mismatches 159;
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Unpublished (2001)
                            125 CTATAAGATTTTCCAGTAATAGAAATGACTTTAGAATGATGAACCAAGCGGTCCAATAAA 184
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription
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                                                                                   GCAGAAGTAAGCCGGTTATCACCAAATATACGATTCCATTGACCAAATTCTAAGTTTGAA
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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Tel: 650 723 2227
Fax: 650 725 8221
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Department of Biological Sciences
Stanford University
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Plate: 1118078 column: 2
Class: transposon-tagged.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH108"
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/clone_lib="lil8" | RescueMu Grid S" | /clone_lib="lil8" | Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transpason designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'www.zmdb.iastee.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Sases 1 to 429)
Walbot, V.
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                                                                                         Maize genomic sequences found using engineered RescueMu Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/cultiva==mmixed background W23/A188/B73"
/db_xref==taxon:4577"
/db_trisue_type="leaf"
/dev_stage="adilt"
/lab_host="DH10B"
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                                                                                                                                                                               855 California Ae, Palo Alto, CA 94304,
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@eranford.edu
Plate: 1118039 row: 2
Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 133 TATTAGGTGTCTTAAAAATAAGGACTATATAAGGAGTGAAAAAGATGAGTCCATATCAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCTTTTGCAAATAATCGGGATATGTCTACTATGTCTTGGAATG--ATTGTCAGGGAAT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :::|: | | | :::|: | | 619 ATWDRTDAWWADAAWWTTDTDTDDWDKRDRRRKGARRRRTTARAAWDWWTWKAWDWAK 620
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                                                                                                                                                                                                                                                      13 ATAAAGAGAAGGTTTAAAAAATCAATACCTCACCAAAAATAATGGGTTTATTTGTAGAAA
                                                                                                                                                                                                                                                                                                                           CATTGTTACAGGAATACATTGGGGTACTACGAATATATAGAAAGACACCTAACATATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ATAAAAATGAATATGAAATATGGAATCCTCATCGAATAACACAAATACGCCAAACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 KRADDKRDAADRDDAATWTTWTTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDRDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AATTCGTAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAA
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                                                                                                                                                                                     Length 1101;
                                                                                                                                                                             Query Match
1.3%; Score 75.8; DB 10; Length
Best Local Similarity 18.0%; Pred. No. 1.3e-05;
Matches 123; Conservative 286; Mismatches 274; Indels
                    1. .1101
/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROSK10"
/clone lib="RPCT-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTWTTWTATTTATTTTWTTTWTA 415
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     Location/Qualifiers
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/db xrefe="taxon:33085"
/clone="EINDD.21"
/clone="EINDD.21"
/clone="EINDD.21"
/clone="bib="EI_10" 12 KB"
/clone="bib="EI_10" 12 KB"
/note="Vector: pH052; Site 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens from early log phase trophozoites of E. invadens medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of EnA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pH052."
                                                                                                                                   BZ388480 670 bp DNA linear GSS 30-APR-2003
EINDL21TF EI_10_12_KB Entamoeba invadens genomic clone EINDL21,
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Tel: 301-838-3543
Fax: 301-838-0208
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49.2%; Pred. No. 0.00023;
tive 0; Mismatches 190; Indels
                                                                                                                                                                                                                                                                         Bukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 670)
Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Bollen,K., Hall,W., Anderson,I. and Loftus,B. Gene discovery in the Entamoeba invadens genome Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .670 / Corganism="Entamoeba invadens" /mol type="genomic DNA" strain="IP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brendan Loftus
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                   4018 CATTGCGAAAAATAAAA 4034
                                                                                                                                                                         genomic survey sequence.
                                     BZ388480.1 GI:30235017
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Best Local Similarity 49.29
Matches 184, Conservative
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                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
Tels 650 723 2227
Fax: 650 725 8221
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                                   363 bp DNA linear GSS 10-NOV-
- RescueMu Grid S Zea mays genomic, genomic
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                                 linear
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llarity 51.4%; Pred. No. 0.00011;
Conservative 0; Mismatches 154;
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                                 CG807311
1118080F01.y1 1118
                                                                survey sequence.
CG807311
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Best Local Similarity
Matches 163; Conserv
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/mol_type="genomic DNA"
/culfivar="genotype A17"
/db xref="taxon:3880"
/clone="37K3"
/clone=lib="mth2"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Cook, D.R. and Kim, D.J. unpublished"
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Tel: 301-838-3523
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                                                                                                                                                                                                                                                                              Town, C.D., Shetty, J., Koo, H. and Feldblyum, T.F. Sequencing of BAC ends from Medicago truncatula Unpublished (2003) Other GSSs: MBEEE62TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2%; Score 69.6; DB 10; Best Local Similarity 50.6%; Pred. No. 0.00028; Matches 168; Conservative 0; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4062 ATAACATAAGCTTTACAAATAACGGACATATT 4093
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                                                                                                                                                               Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 301-838-0208
Email: cdtown&tigr.org
Seq primer: CAGGAAACAGCTATGACC
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                          CG957658.1 GI:39875500
                                                                                                                                                                                  Medicago truncatula
                                                                                      Burvey Bequence.
CG957658
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                                                                                                                                                                                                                                                                              CR479976 580 bp DNA linear GSS 17-NOV-2004 mth2-190L1RM1 BAC end, cultivar Jemalong A17 of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delirect Submission
Submitted (10-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr | Location/Qualifiers
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
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/clone_lib="MTH2"
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llarity 50.6%; Pred. No. 0.00027;
Conservative 0; Mismatches 164; Indels 0
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                                                                                                                                                                                                                                                                                                                   truncatula, genomic survey sequence.
CR479976
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Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                            CR479976.1 GI:48641552
                                                                                                                                       4122 AAGGAGATTTTTT 4135
                                                                                                                                                                              243 TATTATATATAT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago.
1 (bases 1 to 580)
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CR479976
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δ 유 ò g ઠે a ઠે 셤 ò g à survey sequence.

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/organism="Zea mays"
/mol type="genomic DNA"
/cullivar="mixed background W23/A188/B73"
/db xref="taxon:457""
/fisue type="leaf"
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/doct="DH108"
/clone lib="1118 - RescueMu Grid S"
/clone lib="1118 - RescueMu Grid S Mu Lransposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.randb.iastate-edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmide. DH108
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3881 TCTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGCATTCCGGTTGCACA 3940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon topublished (2001)
Conteat: Walbot Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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AG-ND-138G17.TR ND-TAM Anopheles gambiae genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 68.6; DB 10; Length 379; 50.8%; Pred. No. 0.00042; ive 0; Mismatches 159; Indels 0
                                                                                                                                                                                                                   855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Bmail: walbotgetanford.edu
Plate: 1118077 column: 2
Class: transposon_tagged.
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                                                                                                                                                                                                   Stanford University

    (bавев 1 to 379)
    Walbot, V.

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Matches 164; Conservative
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BH391984
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rogids, eurosids 1, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Cook, D.R. and Kim, D.J. unpublished"
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                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: CAGGAAACAGCTATGACC
Class: BAC ends.
                                                                                                                                                                                                                   Town, C.D., Shetty, J., Koo, H. and Feldblyum, T.F. Sequencing of BAC ends from Medicago truncatula Unpublished (2003)
Other GSSS: MBEHO/3TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 69.6; DB 10;
ilarity 50.6%; Pred. No. 0.00029;
Conservative 0; Mismatches 164;
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                                                                Medicago truncatula (barrel medic)
Medicago truncatula
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                       CG937914.1 GI:39810051
                                                                                                                                                                          Medicago.
1 (bases 1 to 891)
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es 168; Conserv
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CW960936 linear GSS 21-DEC-2004 AIAA-aac14d08.bl Ancylostoma caninum whole genome shotgun library (AIAAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
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Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Taagareishvili,R., Ronko,I., Wartin,J., Wylie,T., Danie,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R. Gerome Survey sequences from the parasitic nematode Ancylostoma
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library (AIAAGSS 001)"
/note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1;
Ancylostoma caninum genomic DNA was randomIy sheared,
end-repaired and size fractioned to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mtm]nh@gwumc.edu) at George Washington University.
Geoutering by Washington University Genome Sequencing
Center, St. Louis, MO."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University in St. Louis
Washington University School of Medicine
Mathy Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu) DNA
sequenced by Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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1.1%; Score 68; DB 10; Length 735;
Best Local Similarity 50.3%; Pred. No. 0.00064;
Matches 167; Conservative 0; Mismatches 165; Indels
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                                                                                                                4107 CCTTAATTCTAAAATAAGGAGATTTTTTT
                                                                                                                                                           db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
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                                                  648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 1543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEGT strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas ARM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3807 GTTATAATGGAAATTATAATCAAAATACTAGCGATGTGTATTACCAAGGGTATACAAACA 3866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3927 ATTCCGGTTGCACATGTAACCAAGGCATAACTCTGGCTGTACATGTAATCAAGGATATA 3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.

(Culicidae; Anopheles; Anophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3867 ACTATAACCAAGACTCTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGC
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50.1%; Pred. No. 0.00059;
ive 0; Mismatches 193; Indels
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strain="PEST"

/db_xref="taxon:1165"

/clone="A00-13617"

/clone="A00-TAM"

/note="Vector: pECBAC1; Site_1: HindIII"
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AG-ND-138G17, genomic survey sequence
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                                                                    BH391984.1 GI:17338125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partial digest.
Seg primer: M13 Rev
Class: BAC ends.
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Best Local Similarity 50.1<sup>s</sup>
Matches 195, Conservative
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/deve_type="leat"
/dev_tage="leat"
/dev_tage="adult"
/lab_host="bHl00"
/clone_lib="ll18 - RescueMu Grid S"
/clone_lib="ll18 - RescueMu Grid S"
/clone_lib="ll18 - RescueMu Grid S"
/note="Grgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total agenomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.radb.iastate.edu' and follow the links for reconserved. RescueMu. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII; and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3762 ATGATAACAATAATAACCTGCACACGGGTAATATGTATGAGCAAAGTTATAATGGAAATT 3821
                                                                                                                                                                                                                                                                                GSS 10-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                          4685 TCCCAGTTCCAGGAGATCCAAGTAATAAAAGATTTTGTTTCCCTTCAAAAAATCGCAAT 4743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG807096 302 bp DNA linear GSS 10-NOV-
1118077G01.y1 1118 - RescueMu Grid S Zea mays genomic, genomic
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                                                                             95 TCCCCACACTGATGGCCCCAGTAATACGATATTTTCATTACGTTCTATGAAGCTGAGT
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Pred. No. 0.00066;
0; Mismatches 99; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="tasno:4577"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
Stanford University
SES California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: wallot@stanford.edu
Plate: 1118077 column: 2
Class: transposon-tagged.
Location/Qualifiers
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Walbot, V.
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Best Local Similarity 56.2<sup>3</sup>
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                      survey sequence.
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A2935561 398 bp DNA linear GSS 16-SEP-2002 M028 E. coli C1845 library subtracted from E. coli MG1655 Escherichia coli genomic clone M028, genomic survey sequence.
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Escherichia coli
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Enterobacteriaceae; Escherichia.

1 (bases 1 to 398)
Elanc-Poctard, A., Tinsley, C., Scaletsky, I., Le Bouguenec, C., Guignot, J., Servin, A.L., Nassif, X. and Bernet-Camard, M.
Representational difference analysis between Afa/Dr diffusely adhering Escherichia coli and nonpathogenic E. coli K-12
Infect. Immun. 70 (10), 5503-5511 (2002)
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                                                                                                  1002 AAATAAGAATCAACATCATTGCGAAAAATAAAAACCTACTCACAAAATCTATTGCATATC
                                                                                                                                                           CGTAACAGTCGGCAATAATATGAAATAGGAGCTCCGCTCCTTGCTTTTGAAATGGTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 CGAACGITICAICCCACTGCCCGAACGGCAGATIGGATGTCAGGATCATIGCGCTCTTTT
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Class: representational difference analysis.
Location/Qualifiers
1. .398
| organism="Escherichia coli" | /mol_type="genomic DNA" | /mol_type="genomic DNA" | /mol_train="Class" | /db_xref="taxon:562" | /db_xref="taxon:562" | /clone="MO28" | /clone="MO28" | /clone="lib="E. coli Cl845 library subtracted from E. /mg1655" | /dlone="mode" | /clone="mode" | /clone="mode"
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                                                                                                                                                                                                                                         4062 ATAACATAAGCTTTACAAATAACGGACATATT 4093
                                                                                                                                                                                                                                                                                                        ATAATAATAATAATAATAATAATCATAAT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92296, Chatenay-Malabry cedex, France
Tel: 33 1 46 83 58 43
Fax: 33 1 46 83 58 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Faculte de Pharmacie Paris XI
92296, Chatenav-Malahm
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Schmidtea mediterranea clone HB.22.5c unknown mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3723 TITATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACCTGC 3782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3843 TGTATTACCAAGGGTATACAAACTATAACCAAGACTCTAGTAATGTATAATCAAA 3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3663 TAGAGGTATTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAGGTACAT 3722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3783 ACACGGGTAATATGTATGAGCAAAGTTATAATGGAAATTATAAACAAAATACTAGCGATG 3842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3903 ATTATACTAACAATGACCTGCATTCCGGTTGCACATGTAACCAAGGGCATAACTCTG 3962
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                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alvarado, A.S., Newmark, P.A., Juste, R.B. and Robb, S.M.C. Direct Submission
Submitted (07-DEC-2001) Neurobiology & Anatomy, University of USCHOOL Of Medicine, 50 North Medical Drive, Salt Lake City, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ATGAATGGAAGGTAACATATGACTACAAAATTTAAAAATACATCAACTTTATAAAAATAA
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1 (bases 1 to 679)
Alvarado, A.S., Newmark, P.A., Robb, S.M.C. and Juste, R.B.
The Schmidtea mediterranea database as a molecular resource studying platyhelminthes, stem cells and regeneration levelopment 129 (24), 5659-5665 (2002)
231 ATAATTATATATTATAGTTATAATTATAATTATAA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.1%; Score 67; DB 4; Length 679;
Best Local Similarity 45.1%; Pred. No. 0.0011;
Matches 235; Conservative 0; Mismatches 286; Indels
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| Organism="Schmidtea mediterranea"
| | Mol Lype="MRNA"
| | Strain="CIW4"
| | db_xref="taxon:79327"
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4083 ACGGACATATTCTAGAAGAGGTCTCCTTAATTCTAAAATAA 4123

631 ATAATAATAATAACTAATANTNATAATAATAATAATTA 671

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expression cassette; transformation; transgenic; plant; bacteria;
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pesticidal activity.
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20-FEB-2003; 2003US-04488633P.
20-FEB-2003; 2003US-0448863P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2003US-0448810P.
19-FEB-2004; 2004US-007812P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782040.
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782191.
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 Bacillus thuringiensis.
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Adr84199 Bacillus
Adr891003 Sequence
Adr901003 Sequence
Adr901013 Sequence
Adr89418 Bacillus
Adr89418 Bacillus
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                                                                                              December 19, 2005, 09:48:39; Search time 2211.9 Seconds (without alignments) 18018.361 Million cell updates/sec
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                                                                                                                                                                                               Description
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
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Result No.

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                                                                                                                                                                         Claim 1; SEQ ID NO 12; 178pp; English.
                                Koziel MG,
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Best Local Similarity 100.0%;
Matches 5980; Conservative 0;
                              Hargiss T,
(ATHE-) ATHENIX CORP
                                                            WPI; 2004-635574/61.
P-PSDB; ADR89402.
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1621 GTGTTGTATATGGAAACTCCAGAGTTAACGTATATGGTTGGACACATACAAGTTTAAAAC 1680 AGATAAAACAGGGGGGGCACAGTGCTGACACTTGCTCGAAATTTAATAAATTTCGTAGAG 1020 960 720 780 780 900 900 841 CGGAATTAATATCACCTAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAA CTACCGCTAGACCAGAGTATCGTGTTTTCAAAGGCAGATTTTCGTAGGGTAGGGGACCTG TTAAACTTTCAGAAAGAGATTTCAATGAAATTCTAGGAGGGTCATTGTCAAGAAACAATG AGATAAAAACAGGGGGGGGACAGGTGCTGACACTTGGTCGAAAATTTAATAAATTTCGTAGAG GTAACGGTATTTTTCAACGTATGTCTGGAACTACGAGTAATGATCTACGTAATAGATT TTCAGAATGCCGATGTATATAAAATTACTTCATTAGCTATCATGAACCTAGTAGGAGAGA CACTTGTATTGCACTCTAATGGTGTTAGAGGACCCTCTCATAGATTATCAAATGCGGCAT GIGTIGIATATGGAAACTCCAGAGTTAACGTATATGGTTGGACACATACAAGTTTAAAAC AAGACGGTAAACCACTTCAAAAAGACAAATAATTCTGATATCGGACAATTAGTTTATTATT crcaagrarrgrrarraccracrrrrgcacaagcrgcaargrgcagrrarracrarraa GGGATGCAGTTCAATATAAAGCACAATGGTTCCCATTTTTGAGTGCAGAGAATGTAAGAT AAAIGACGITGGCGGIATIGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAAT 141 CATCGGGAACTTATAGTTACGGAATTGGCCTAATACTTTTAATGGGTTAGAGGCTA ATGITTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAAGACTACACAAAGG GTAACGGTATTTTTCAACGTATGTCTGGAACTACGAGTAATGATCTACGTAATATTGATT CTACCGCTAGACCAGAGTATCGTGTTTCAAAGGCAGATTTTCGTAGGGTAGGGGACCTG ATTTAAATTATGATGCAGGTAATAATGGGCTAAGCAGGATGACAATTGAATCTACGTTCC CTCAAGTATTGTTATTACCTACTTTTGCACAAGCTGCAAATGTGCAGTTATTACTATTAA CGGAATTAATATCACCTAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAA ATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGATGCAGTGGGATATT CATCGGGAACTTATAGTTACGGAATTGGCCTAATACTTTTAATGGGTTAGAGGCTA 1561 1561 1621 ઠે

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AXMI-008 alternative start site coding sequence
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34.7%; Score 2073; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2073; Conservative 0; Mismatches
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20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782036.
19-FEB-2004; 2004US-00782036.
19-FEB-2004; 2004US-00782036.
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                                                                                                                                                                                                                                                                                                                      Bacillus thuringiensis.
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ò :	237 AATACGCCAAACAGATATCCTTTTGCAAATAATCGGGATATGTCTACTATGTCTTGGAAT 296	& a	1317 AAGGGTAACGGTATTTTCAACGTATGTCTGGAACTACGAGTAATGATCTACGTAATATT 1376
	MARGOCCAMACAGNIALCCIIIGCAMAIDAICGGGANIALGELLIACLAIGICLE GATTGTCAGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAA GATTGTCAGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAA GATTGTCAGGGAATCTCATGGGAATTTGGGAATCGAAACGAAAACAATAAAAA	ъ _е	1377 GATTITCAGAATGCCGATGTATATAAAATTACTTCATTAGCTATCAACCTAGTAGGA 1436
	GGGATAAATCTTATAGACTTTGTGATAGAACCTAGGTTTGGGTGGAATTAATAGACTATA	& 8	1437 GAGACTACCGCTAGACTATCGTGTTTTCAAGGCAGATTTTTCGTAGGGGGGA 1496
	TCAATAATAGGAAACTAATTCCGACTAATCGTCAAACTGTGTCAGCACTTTCTATGT 	& a	1497
		& A	1557
		ර සි	. 1617
	CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATTCTGATATCGGACAATTAGTTTAT 65 	& a	1677
		ò 8	1737 TACCTTCAAAATTATCTTGCTAATGCCTATACCTATGTAATAAAAGGCACTCATACAGGT 1796
	TACTA TACTA	ò a	1797 GGGGATTAATCCGTTTTTAAGAACAAATCAGAGTATAACGCAGTTTATGCAGGTGGC 1856
	ATGTA 	ờ a	1857 GGAATTAGATTATTAATAACAAAACTGCAGGACAAAGTTACCGTATTCGTTTTCGT 1916
	AGCGA HGCGA	δ a 	
	STTTA 	<i>∂</i> 8	1977 AATCGTTTTGTATCGCTTGAAAATCTTACTCTGGAAATTATGACGATTTAAAATATGGT 2036
	aatcagataaaacagggggggacaggtgctgacacttggtcgaaatttaataaatttcgf 	& € 	2037 GATTTTAAATTCGCTGAAATTATCACACCTCCATTACCTAGTTCAACATTCAGATGGAT 2096
	TTGAG TTGAG	<i>></i> 옵	97 GTGGAGATGCAAGCGAATAGTTTTCAATCAGAI
	1077 AAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGATGCAGTGGGA 1136 	<i>장</i> 名	1 1
	GGTTAGAG GGTTAGAG	<i>&</i> €	2217 AAGAACGCGGTGAACGATTTACCAATTAA 2249
	1197 GCTAATGGAACACGGGGACCTGGTTTACTTACTTAGGTTAGGAAATAGGTATATATA	AR AD	NULT 4 889405 ADR89405 standard; cDNA; 1686 BP.
	1257 GAGTATCTTTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAAGACTACCA 1316 		XX XX XX DT 18-NOV-2004 (first entry)

480

360

2908

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900

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2369 GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 2428

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CAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAA 3508
                                                                                                                                                                   181 CTCCAAAATGGAGACTTTTCTGGGAATGATTGGACATTTCGGAAATTGGACATTTCGGAAATGATTATCATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 GAGTTACACTATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTCG
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                     GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA
                                                                                                     CCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGG
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                                                                                                                                                                                                                                                       241 TCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATAT
                                                                                                                                                                                                                                                                                                               GGAACTCTATTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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                                      88; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
spression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
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100.0%; Pred. No. 2.8e-297;
tive 0; Mismatches 0;
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1. .1686
/*tag= a
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2003US-0448812P.
2004US-00781979.
2004US-00782020.
2004US-00782046.
2004US-00782141.
2004US-00783141.
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2003US-0448633P.
2003US-0448797P.
2003US-0448806P.
AXMI-008orf2 coding sequence.
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Matches 1686; Conservative
                                                                                                                                         Bacillus thuringiensis.
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                                                                                             The present invention relates to modified insecticidal Bacillus thuringiensis crystal proteins Cry4Ba and Cry19Aa which have enhanced toxicity against a variety of insects, e.g. meaguitos and legidoptera. The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. The present sequence is the coding sequence of the wild-type Cry19Aa protein, which can be modified with: a substitution of amino acids at positions 355 through 358 with amino acids tyrosine, glutamine, aspartic acid, and leucine; an insertion of at least one amino acid (e.g. arginine) after position 358 and a deletion of the amino acids at positions 414 through 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGACAAAATTGAATTCCTCCCAAGTA----ATACAACAACTTTAGAATATGAGGGAGAA
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      New modified Bacillus thuringiensis insecticidal crystal proteins (i. Cry4Bs and Cry19As) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.
                                                                                                                                                                                                                                              Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;
                                                                         Disclosure; SEQ ID NO 4; 63pp; English.
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Best Local Similarity 74.8%;
Matches 1296; Conservative (
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Gaps

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AXMI-008 full length coding sequence.

(first entry)

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New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, generating altered or improved delta-endotoxin or delta-endotoxin associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or
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                                                                                                           ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance;
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                                                                                                                                                                                                                          Location/Qualifiers
127. .2145
/*tag= a
/product= "AXMI-008"
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448805P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-0078205.
19-FEB-2004; 2004US-0078205.
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                                                                                                                                                                                           Bacillus thuringiensis.
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ADR89413 standard; cDNA; 2145

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                                                                                                                                                                                                                                                                              2832 ATCATTAGATAATTTAGAAGTAATTGAAGAAGGGCCAATAGATGGGGAAGCACTGTCACG 2891
                                                                                                                                                                                                                                                                                                                                                                                                                      3252 ACAACAATAGATGGTGTTTCTGTATTGGTTCTAATTGGAGTGCTGGCGTATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3628 CACTICITGCGAAGAAGGATATATGACAAAAACAGTAGAGGTATTCCCAGAAAGTGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3492 TGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGCATTGAATTAAT
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                                                                                                                  2772 racaaatgaaaararaggggrirrggfcargriraaaararcirciccagarggaracc
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                                                                                                                                                                 2974 TACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGC
                                                                                                                                                                                                                                            3034 TACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACA
                                                                                                                                                                                                                                                                                                                       TGTGAAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAAACACA
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                                                                                          GCATGTGAAGTGTCACGATCGTCCATTTGATTTTCATATTGACACCGGAGAAGTAGA
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                                                                                                                                                                                                                                                                                                                                                                           This gene is ligated to a promoter region enabling expression in Cyanobacteria and the resultant chimeric gene is used to produce Bacillus thuringiensis 8 (Bt 8) protein. A truncated form of the protein can also be produced using a shorter gene. Transformed cyanobacteria and their progeny can be used in insecticidal compsns., esp, for controlling mosquitos. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGGAAGAAATTGATGCCATCATGAATGTTCCAGCTGATTTAAACTATCTGTATCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                  Chimeric gene for expression in Cyanobacteria – contg. DNA fragment coding for insecticidal active protein produced by Bacillus strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3684 BP; 1302 A; 585 C; 693 G; 1103 T; 0 U; 1 Other;
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13.2%; Score 790.6; DB 1;
Best Local Similarity 71.4%; Pred. No. 2.7e-134;
Matches 1093; Conservative 0; Mismatches 414;
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                                                                                                                                                                                         Mcintosh
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page ?; 50pp; English
                                     88WO-US000734
                                                                         87US-00021405
                                                                                                          (UNMS ) UNIV MICHIGAN STATE.
(PLAN-) PLANT GENETIC SYST.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                       Chungjatup W,
                                                                                                                                                                                                                           WPI; 1988-271170/38
                                                                                                                                                                                                                                            P-PSDB; AAP82314
                                     03-MAR-1988;
                                                                         04-MAR-1987;
07-SEP-1988
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Novel chimeric gene expressed in cells of Cyanobacterium for controlling mosquitoes in water, comprises a DNA fragment comprising promoter region and a DNA fragment containing gene encoding for insecticidal protein.
                                           Toxin; Bt8; insecticidal; cyanobacterium; synechocystis 680; endotoxin; mosquito control; glutamine synthetase inhibitor; inoculum; gene; ds.
                                                                                                                                                                                 protein"
                      thuringiensis variant israelensis toxin (Bt8) gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxin (Bt8) protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                       /*tag= a
/standard_name= "Shine-Dalgarno (SD) Sequence"
/note= "Consensus ribosome binding site"
/*tag= b
                                                                                                                                                                             /product= "Bacillus thuringiensis toxin (Bt8)
/transl_except= (pos:1708. 1710, aas:Ger)
/transl_except= (pos:2356. .2358, aa:Gln)
/transl_except= (pos:3067. .3069, aa:Gln)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 3684 BP; 1301 A; 587 C; 694 G; 1102 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Mcintosh L;
                                                                           Bacillus thuringiensis serovar israelensis
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 2a; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                              Chungjatupornchai W,
                                                                                                                                                                                                                                                                                   92US-00837625
                                                                                                                                                                                                                                                                                                                  88US-00243798
                                                                                                                                                                                                                                                                                                                                        (UNMS ) UNIV MICHIGAN STATE
08-MAY-2002 (first entry
                                                                                                             145. .149
                                                                                                                                                                                                                                                                                                                                                                                     2002-163196/21.
                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU76029.
                                                                                                                                                                                                                                                                                  18-FEB-1992;
                                                                                                                                                                                                                                                                                                       04-MAR-1987;
13-SEP-1988;
                                                                                                                                                                                                                                       US6335008-B1
                                                                                                                                                                                                                                                            01-JAN-2002
                                                                                                                                                                                                                                                                                                                                                             Vaeck MA,
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fragment having a promoter region, for expression of a Cyanobacterium such as Synachocystis 680. The gene comprises a DNA fragment having a promoter region, for expression of a DNA fragment in the Cyanobacterium, and a fragment coding for an insecticidally active protein endotoxin produced by Bacillus thuringiensis, B. sphaericus or B. kurstaki strain, or for a truncated form of the protein. Cyanobacterium is useful for controlling mesquitoes in water by applying the bacterium of the bacterium of the bacterium of the bacterium of express the bar gene are selectively protected against competing nontransformed Cyanobacteria by treating the region with glutamine synthetase inhibitors. The invention is useful as viable incolumn to promote the growth of mosquito larvae. Cyanobacterium provides better control of mosquitoes, ensures a long-term destruction of mosquitoes, guarantees direct uptake of the bacterium by the mosquitoes and assures more stable availability of the toxin in the vicinity surface since it is self replicating and floats at or near the water surface. The present present invention relates to a new chimeric gene expressed in cells self replicating and floats at or near the water surface. The present nucleic acid sequence encodes the B. thuringiensis variant israelensis toxin (Bt8) procesin of the invention (malelane)

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                                                                  TTTACTAGAATAGGTGGTATTGCTGTTTAACAAATAAGCGAAAAAGGTTGTGAGTCCTAT
                                  Gaps
                                24;
   Length 3684;
                                Indels
13.2%; Score 789; DB 6; L ilarity 71.3%; Pred. No. 5.2e-134; Conservative 0; Mismatches 415;
                 Similarity
                 Best Local Sım.
Matches 1092;
                                                                  2260
 Query Match
Best Local 8
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2064 İGTATTAGATGAGACAGAGAACCAAAATTTAGAATCAGAACGAGAAGTTGTGAATGCACT

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2303 2423 2673 2483 2793 2853 2651 2913 2771 3033 2831 3093 2891 3327 2544 redecandantrearecentendanterrechectentraactareretarecente 2603 ACAAGCATATGATGTAGCGAAACAAGCCATTGATGCTTTATTCACAAATGTACAAGATGA 3011 3132 TGTAGAGTTGGATGCACGGGTGGCACAAGCGCGCTATTTGTATACAAGAAATATTAT 3191 GTTTACAAATGACGCGAAAGATGCATTAAACATTGGAACGACAGATTATGACATAGATCA ACCCCAAAICTIGIGGAAIGIATITCTGAAGAAITATATCCAAAAGAAAAAIGCTGT **ATGGGATGAAATAAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGG** 3012 GGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTAGGTGGTATTTGGTACCATC ATTAGATGAAGTTAAAAATGCGAAACAACTTAGTCAATCTCGAAATGTACTTCAAAACGG AGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAA 3034 TACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACA TGTGAAACAAAAGGAAAAGGAAATGGAAACACACATGGAGAAAAAACGTTGGGAAACACA 3328 ICAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGTGCACGAAATGTCAT GTTTACAAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCA AGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATGTT 2304 GGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACAATTGAAGAAGA TAATCCTATTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAAC 2364 IGATCCTATTTTAAAGGGCATTACCTTCATATGTCTGGGGCGAGAGACATTGATGGTAC TCTATTTCCAACCTATATCTGTCAAAAATAGATGAGTCTAAAATTAAAACCATATACACG 2424 GATATTTCCGACCTATATATTCCAAAAATTGATGAATCAAAATTAAAACCGTATACACG TTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAAATTTAATGGTAACACGTTA 2484 TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAAGATGTAGAACTAGTGGTTTCACGCTA 2734 CGGGAAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAA TAC------CTTTGATTGTGAAGGGTCTAATCGTTGAGACGTCCGCTGTGCC 2652 GGCTAACATTGGGAACACTTCTGATATGTTGTATTCATGCCAATATGATACAGGGAAAAA GCATGTGAAGTGTCACGATCGTCATCTTTGATTTTCATATTGACACCGGAGAAGTAGA TACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGC 2772 TACAAATGAAAATATAGGGGTTTGGGTCATGTTTAAAATATCTTCTCCAGATGGATAGCGC 2832 ATCATTAGATAATTTAGAAGTAATTGAAGAAGGGCCAATAGATGGGGAAGCACTGTCACG ACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGA---3268 GATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATA TCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCC ---GTTACACTATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTC 2124 2184 2440 2244 2500 2554 2614 2794 2604 2712 2974 3094 3154 2952 3072 2320 2380 2674 2914 3211 요 쉱 g g g 요

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toxicity against a variety of insects, e.g. mosquitos and lepidoptera. The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. The present sequence is the coding sequence for the wild-type Crydsa protein, which can be modified as follows: the amino acid aspartic acid at position 454 is substituted with, for example proline, glycine, alanine or threonine, and at least two or more additional amino acids are substituted amino acids inserted after the substitution, where the amino acids inserted after the substitution, where the amino acids inserted after the substituted amino acid at position of 454 and valine. In addition, the modified Crydsa protein may comprise the following substitutions: Thr456 is crydsa protein may comprise the following substitutions: Thr456 is with alanine; lle580 is replaced with alanine, phenylalanine or tyrosine; Ile581 is replaced with alanine, phenylalanine or tyrosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2772 TACAAATGAAAATATAGGGTTTGGGTCATGTTTAAAAATATCTTCTCCAGATGGATACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2484 TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTGGTTTCACGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2734 CGGGAAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2364 IGATCCTATTTTAAAGGGCATTACCTTCATATGTCTGGGGCGAGAGACATTGATGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2712 GCATGTCGTATGTCAGGATTCCCATCAATTTAGTTTCACTATTGATACAGGGGCATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                              2064 TGTATTAGATGAGACAGAGAACCAAAATTTAGAATCAGAAACGAGAAGTTGTGAATGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCGGCCATTTCTATAGAATGTATGTCAGATGAAAAAATCCTCAGGAAAAAATAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2500 AGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2554 TAATCCTATTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2614 TCTATTTCCAACCTATATCTGTCAAAAATAGATGAGTCTAAATTAAAACCATATACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2544 TGGGGAAGAATTGATGCCATCATGATGTTCCAGCTGATTTAAACTATCTGTATCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAC------CTTTGATTGTGAAGGGTCTAATCGTTGTGAGACGTCCGCTGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATGTGAAGTGTCACGATCGTCCATTTGATTTCATTTGACACCGGAGAAGTAGA
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                                                                                                                                                                                                                                                                                                                                                                          2260 TITACTAGAATAGGTGGTATTGCTGTTTAACAAATAAGCGAAAAAGGTTGTGAGTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTACAAGTAGTAGGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2124 GITTACAAATGACGCGAAAGATGCATTAAACATTGGAACGACAGATTATGACATAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCGCAAATCTTGTGGAATGTATTTCTGAAGAATTATATCCAAAAGAAAAAATGCTGTT
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                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                      Length 3684;
                                                                                                                                                                                                                                                                    Sequence 3684 BP; 1302 A; 587 C; 692 G; 1103 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                    Score 789; DB 14;
Pred. No. 5.2e-134;
0; Mismatches 415;
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Best Local Similarity 71.39
Matches 1092; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified Bacillus thuringiensis insecticidal crystal proteins (i.e. Crysta and Cry19Aa) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.
                                                                                                                                                                 CACTICITGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTATTCCCAGAAAGTGATCG
                                                                                                                                                                                                                                                                                                             TGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGCATTGAATTAAT
                                    TAAAAATGGTGATTTTACACAAGGGGTAATGGGGTGGCATGTAACTGGAAATGCAGACGT
                                                                                                                                             AAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAGAAGG
                                                                                                                                                                                                                                       The present invention relates to modified insecticidal Bacillus thuringiensis crystal proteins Cry4Ba and Cry19Aa which have enhanced
                                                                                             ACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTT
     <u>AACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGT</u>
                                                                       ACAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis Cry4Ba coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triccardadecagigarranarananahiahe 3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cry4Ba; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                               TIGTATGCAAGGATATGATAACAATAATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
157. .3567
/*tag= a
/product= "Cry4Ba"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein gene has high insecticide activity to diptera larvae such as aedes. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2517 CAAGTGATAATATCACAATTCAAGAAGATGATCCTATTTTTAAAGGGCATTACCTTCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2292 AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                          Insecticide protein gene - from Bacillus thuringiensisulaelensis
strain, used to produce protein toxic to diptera larvae, eg. aedes
                                                                                                                                                                                                                                                                                                                                                                                                      30,
                                                                                                                                                                                                                                                                                                                                             Sequence 4065 BP; 1471 A; 595 C; 752 G; 1247 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.0%; Pred. No. 5.3e-134;
Matches 1171; Conservative 0; Mismatches 520; Indels 3
                                                                                                                                                                                                                                                                  Fig 2; Fig 2-1 to 2-3; 8pp; Japanese.
                                                                           87JP-00238394
                                                                                                        87JP-00238394
                                                                                                                                  (SUMO ) SUMITOMO CHEM IND (MARU-) MARUBENI KK.
                                                                                                                                                                               WPI; 1989-134798/18.
P-PSDB; AAP93308.
                JP01080294-A
                                                                           21-SEP-1987;
                                                                                                        21-SEP-1987;
                                               27-MAR-1989
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                2832 ATCATTAGATAATTTAGAAGTAATTGAAGAGGCCAATAGATGGGGGAAGCACTGTCACG 2891
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                                                       3012 GGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTATTTGGTACAATC
                                                                                                                                                                                                                                                                                            TCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATGATGCACGAAATGTCAT
                                                                                                                                                                                                                                                                                                                       3132 iGTAGAGTIGGATGCACGAGTGGCACAAGCGCGTTATTIGTATGATACAAGAAATATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTATGCAAGGATATGATAACAATAATAAC 3778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
461. .3868
/*tag= a
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(revised)
(first entry)
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23-DEC-1990
15-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-1988;
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16-JUN-1988;
                                                                                                                                                                                                   Sequence of israelensis
                                                                                                                                  25-MAR-2003
27-JAN-1991
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                                                                                                               TTAAAATATCTTCTCCCAGATGGATACGCATCATTAGATAATTTAGAAGTAATTGAAGAAG
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                       ACATGGAGAAAAACGTTGGGAAACACAAAGCCTATGATCCAGCAAAACAGGCTGTAG
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ATTITCATATIGACACCGGAGAAGTAGATACAAATACAAATGTAGGTATTGATGTCTTAT
                                                                                        TAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A toxin active against dipteran insects, having a specified as sequence or a mutant having the same protein secondary structure or, if the structure is altered, having the same biological activity, is claimed. Also claimed is a DNA molecule including a nucleotide sequence encoding the as sequence. The novel toxin gene is toxic to dipteran insects e.g. mosquitos. (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACTTI-----TCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1908 TGTATTAGATGAGAGAGGAACCAAAATTTAGAATCAGAACGAGAAGTTGTGAATGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGATGAAATAAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2260 TTTACTAGAATAGGTGGTATTGCTGTTTAACAAATAAGCGAAAAAGGTTGTGAGTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTTACAAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis toxin toxic to dipteran insects - produced by isolated from Bacillus thuringiensis var. israelensis strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                          toxin gene derived from a Bacillus thuringiensis var. (B.t.i.) microbe identified as strain HD567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 787.4; DB 1; Length 3535; Pred. No. 1e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3535 BP; 1247 A; 573 C; 666 G; 1049 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 416; Indels
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1. .3411
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                                                                                                                                                                                                                                                                                                      Insecticide; diptera; mosquito;
   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87US-00098359.
88US-00207690.
AAN91003 standard; DNA; 3535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.2%;
Best Local Similarity 71.3%;
Matches 1091; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGGAACGACAGATTATGACATAGATCAAGCCGCAAATCTTGTGGGAATGTATTCTGAAG 2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The gene is used to produce protein toxic to diptera larvae, e.g. aedes. Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
                                      3336 TGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGCATTGAATTAAT
                       CACTICITGCGAAGAAGGATATATGACAAAAACAGTAGAGGTATTCCCAGAAAGTGATCG
                                                                                    2292 AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                         larvae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insecticide protein gene - from Bacillus thuringiensisisulaelensis strain, used to produce protein toxic to diptera larvae, eg. aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 781.8; DB 1; Length 4184; 68.2%; Pred. No. 1.1e-132; ive 0; Mismatches 517; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4184 BP; 1501 A; 627 C; 774 G; 1282 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis, israelensis strain; toxin; diptera
                                                                                                                                                                     TTGCATGAACGAGTGATTAATAAAAATACC 3426
                                                                                                                                                TTGTATGCAAGGATATGATAACAATAATAAC 3778
                                                                                                                                                                                                                                                                                                                                                                                      Bacillus thuringiensis israelis strain toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 2(1) - 2(3); pages 639-40; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis; israelensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                           AAN96139 standard; DNA; 4184
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.2
Matches 1173; Conservative
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P-PSDB; AAP93308.
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25-MAR-2003
15-MAY-1990
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GGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACAATTCAAGAAGA 2207
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                                                                                                                                                                                                                                                                                                          TAATCCTATITITAAAGGAAAATITCTACAGAIGCGTGGAGGACGAGACATATATGGAAC
                                                                                           2614 TCTATTTCCAACCTATATCTGTCAAAAATAGATGAGTCTAAATTAAAACCATATACACG
                                                                                                              2268 GATATTTCCGACCTATATATTCCAAAAAATTGATGATGAAATTAAAACGGATACACG
                                                                                                                                                                          GGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTATTTGGTACAATC
                                                              rearcciaritriaaaggecarraccircarargrereggeggggggggacarrearggrac
                                                                                                                                                                                                                                                                                    2794 ICCTICAIGIGGAGATIAICGCTGTGAAICAICGICICAGIAIGIGAGCCAAGGGTAICC
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                                                                                                                                                          TTATCGAGTAAGAGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3388 AACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAAATGGTGATTTTACACAAGGGGTAATGGGGTGGCATGTAACTGGAAATGCAGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTGGAAAAGGTATGTAACGATGATGATTGTAATGGAAAGCAGGAAACACTTAAGTT
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TAICTAATTGGAGTGCTGGCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATG
                                                                                                                                                                                 3645 TCTTACGTGTTATTGCCAAAAAAAAGACCTGGAAATGGGTATGTCACGCTTATGGATT
                                                                                                                                                                                                                                              CAGTAGAGGTATTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAGGTA
                                                                                                                                                                                                                                                                                                                                  CATITITATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAATCAAAATTATACTAACAATGATGACCTGCATTCCGGTTGCACATGTAACCAAGGGC
                                                                    TGTTACGTGTGTGATTGCCAAAAAAAAAGGACCTGGAAAAGGGTATGTAACGATGATGGATT
                                                                                                                                                        GTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGCGAAGAAGGATATATGACAAAAA
                                                                                                                                                                                                                                                                       3840 ATGTGTATTACCAAGGGTATACAAACAACTATAACCAAGACTCTAG-----TAATATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "insecticidal protein"
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   ATGCATTATTTACAAATGAACAAGA-----GTTACACTATCATATTACTTTAGATCATA
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                                                          A plasmid contg. the gene is isolated by forming a gene library from plasmid DNA of B.thuringiensis israelensis (HD 522 strain, USA Goldberg ONR60) followed by screening with anti-israelensis insecticidal protein IG. The insecticidal protein is highly effective against Diptera, esp. Aedes. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGTGATAATATCACAATTCAAGAAGATGATCCTATTTTTAAAGGGCATTACCTTCATA
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                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                            DB 1; Length 4934;
                                                                                                                                                          Sequence 4934 BP; 1797 A; 749 C; 877 G; 1511 T; 0 U; 0 Other;
                                                                                                                                                                                                                         Indels
   etc.
                                                                                                                                                                                        Score 774.6; DB 1;
Pred. No. 2.2e-131;
0; Mismatches 404;
gene library from plasmid deoxyribonucleic acid,
                             Disclosure, Page ?; 9pp; Japanese
                                                                                                                                                                                       Query Match 13.0%;
Best Local Similarity 71.4%;
Matches 1071; Conservative 0
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                  2840 GGCCAATAGATGGGGAAGCACTGTCACGCGTGAAACACATGGAAGAAATGGAACGATC
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                                                                                        2900 AAATGGAAGCAAAACGTTCGGAAACACAACAACAAGCATATGATGTAGCGAAACAAGCCATTA
                                                                                                                                       ATGCATTATTACAAATGAACAAGA-----GTTACACTATCATATTACTTTAGATCATA
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 GACCACTAACAGGTGAAGCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAACAAC
                                                                   ACATGGAGAAAAACGTTGGGAAACACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAG
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1. .3543
/*tag= a
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                                                                                                                                  A library was constructed from Bacillus thuringiensis PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This was sequenced (AAQ81178). A current acrystalliferous B.t. host carrying pMYC1625 produced a 130 kba crystal protein (AAR63078) toxic to calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                        AAACAGTACAACAAATAATTAATACATTTTATGCAAATCCTATAAAAAACACTTTACAAT
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                              Query Match
12.8%; Score 765.8; DB 2;
Best Local Similarity 71.5%; Pred. No. 8.7e-130;
Matches 1058; Conservative 0; Mismatches 397;
                                                 Calliphoridae pests isolates or toxins.
                                                                                                      Disclosure; Page 36-38; 50pp; English.
                                                 Method for controlling
Bacillus thuringiensis
1995-067338/09
                  P-PSDB; AAR63078
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                             ATTCATGCCAATATGATACAGGGAAAAAGCATGTCGTATGTCAGGATTCCCATCAATTTA
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Matches 1057; Conserv
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Sequence 71, Appl
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Sequence No. US20040250311A1

GENERAL INFORMATION:

APPLICANT: Carcia; Nadine

APPLICANT: Roziel, Nicholas B.

APPLICANT: Michael G.

APPLICANT: Carr, Brian

TITLE OF INVENTION: AXM1-008, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for Its Use

FILE REFERENCE: 045600/274147

CURRENT PILLING DATE: 2004-02-20

PRIOR FILING DATE: 2003-02-20

SOFTWARE: FactSEQ for Windows Version 4.0

SEQ ID NOS: 28
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US-10-032-717-3
US-10-032-717-27
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Bacillus thuringiensis
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Matches 5980; Conservative
 LENGTH: 5980
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Db 5701 GAAAACTCTCCATAATCGGAGCGGTTGTAAACCAATTGTTTCGTGTATAACTGACTTTC 5760 Oy 5761 CGTTCAACGTTCCCCTTTCATGCCGCTATAAGGATTACAAGGTTGCACTTCAAGGTTA 5820	RESULT 2 US-10-781-979-2 US-10-781-979-2 Sequence 2, Application US/10781979 Sequence 2, Application US/10781979 Publication Wo. US20040250311A1 GENERAL INFORMATION: APPLICANT: Carcari, Madine APPLICANT: Koziel, Michael G. APPLICANT: Workly Michael G. APPLICANT: Workly Michael G. APPLICANT: Workly Nicholas B. APPLICANT: Workly Nicholas B. APPLICANT: Ouck, Nicholas B. APPLICANT: Ouck, Nicholas B. APPLICANT: Ouch SAMI-008, A Delta-Endotoxin Gene and TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and TITLE OF INVENTION: Micholas B. APPLICANT: Ouch SAMI-008, A Delta-Endotoxin Gene and TITLE OF INVENTION: Mothers: 0/448,797 PRIOR APPLICATION NUMBER: 60/448,797 PRIOR APPLICATION NUMBER: 60/448,797 PRIOR APPLICATION NUMBER: 60/448,797 PRIOR APPLICATION NUMBER: 60/448,797 PRIOR APPLICATION NUMBER: CANANAMER: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 2082 TYPE: DNA ORGANISM: Bacillus thuringiensis FRATURE: FRA	Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 168 GTGAAAAGGTCCATATCAAATAGAATATGAAATATTGGAATCCTCATCG 227
	4921 TCAAAAGGTATTTCATCATAAATGGTCTATAATATAGCTTAAATGCAGTGATTTACAGGCG 4980 4921 TCAAAAGGTATTTCATCATAATGGTCTATAATATAGCTTAAATGCAGTGATTTACAGGCG 4980 4981 TCTTGCAGGTTTCGTTGTATCATAATGAGAATGAACCTTCTAAAGTTGGACAAAGCT 5040 4981 TCTTGCAGGTTTCGTTGTATCATAATGAGAATGAACCTTTCTAAAGTTGGACAAAGCT 5040 5041 TCTGCAGGTTTCGTTGTATCATAATGAGAATGAACTTGAAAGTTGGACAAAGCT 5040 5041 TCGATCATATTGCTGAAACTGTTCGTAATCTATTAAAACAGGTGGCGTAAGGTTTT 5100 5101 CTTGCCATTTTTGTGGATACGTCATTGATTGAATCTATTAAAACTGGAGTTCGTGAG 5160 5101 CTTGCCATTTTTGTGGATACGTCACTTGTTGAATCTGAAATGAGTTCGTGAG 5160 5101 CTTGCCATTTTTTGTGGATACGTCACTTGTTGAATCTGCAAATTGAATACGTAGTTT 5220 5101 CTTGCCATTTTTTGAACTTCTCATTCATTAAAAGTGAATACGAGTTCGTGAG 5160 5161 GAGCTTTTTTCAACCATTCTTCATTCTTTAAAAGTGATATCGAGTTTCGTGAG 5160 5161 GAGCTTTTTTGAACTTCAACCTTGTTAAAGTGTTACCTTATGAAAGAGCA 5280 5161 GAGCTTTTTTGAACTTCAATCCTTTAAAAGTGTTACCTTATGAAAGAGCA 5280 5221 TTTGAATTAAATATTGAATCCTGTTAAACAAGTTTCTTTC	5341 GTTTCTTTTCCCAATCTTCCAAAATCTCTTCCCATAGAATCGGCCTACTCGTGTGCATAT 5400 5341 GTTTCTTTTCCCAATCTTCAAAAATCTTTCCCATAGAATCGGCCTACTCGTGTGCATAT 5400 5401 ACGGTCTGTATTCTGTAAAAATCTTCTCGCCTTCTGCGGTATAAATTGATCCC 5460 5401 ACGGTCTGTTTTTTAAAAAAAAAAAAACAAAAAAAAAAA

10 TCHAINGTGANTTATTATCATANATTCGTAAAAGGGTAACCCGATAGTGTTTAAAGGGTAACCCATAGTGTTTAAAGGGTAACTCTTAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAAA	OY 1608 TCAAATGCGGCATGTTGTATATGGAAACTCCAGAGTTAACGTATATGGTTGGACCAT 1667	1848 GCAGGTGGCGAATTAGATTGATTATAATAACAAACTGCAGGACAAAGTTACCGTATT 1681 GCAGGTGGCGGAATTAGATTGATTATTAATAACAAACTGCAGGACAAAGTTACCGTATT 1681 GCAGGTGGCGGAATTAGATTATTAATAACAAACTGCAGGAGAGATTACCGTATT 1908 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGT 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGT 1768 TGGGGTTCAAATCGTTTGTATGCTGAAAATTCTTTAGTGTATATTATGACGAGGT 1968 TGGGGTTCAAATCGTTTTGTATCGCTTGAAAATTCTTAACTCTTGAAATTATGACGATTAA 1801 TGGGGTTCAAATCGTTTTGTATCGCTTGAAAAATCTTACTCTGGAAATTATGACGATTAA	Qy 2028 AAATATAGTGATTTTAAATTCGCTGAAATTATCACCTTACCTAGTTCAAACATT 2087 Db 1861 AAATATAGTATTTTAAATTCGCTGACTCCTCATTCAACATT 1920 Qy 2088 CAGATGATGTGGAAGCGAACGAATTTCCAACACATTAACCTAGTTCAACATT 1920 Qy 2148 AAAATTGAAGGAATGCAAGCGAATAGTTTCCAATCAGATGTAAACGTGGTTCTCGAC 1980 Qy 2148 AAAATTGAATTCCTCCCAAGTAATACAACAACTTTAGAATATGAGGGAACCTA 2207 Db 1981 AAAATTGAATTCCTCCCAAGTAATACAACAACTTTAGAATATGAGGGAACCTA 2007 Qy 2208 GAAAAAACAAAGAACGGGGAACGATTAACAACTTTACCAATTAA 2249 Db 201 GAAAAAAACAAAGAACGGGGAACGGTGAACGATTAACAATTAA 2249 Db 201 GAAAAAAAAAAAAAAAAAAAAATAAACAACTTTACCAATTAA 2249	RESULT 3 US-10-781-979-4 Sequence 4, Application US/10781979 Publication No. US20040250311A1 GENERAL INFORMATION: APPLICANT: Carcazi, Nadine APPLICANT: Carcazi, Nadine APPLICANT: Carcazi, Michael G. APPLICANT: Aragiss, Tracy APPLICANT: Aragiss, Tracy APPLICANT: Duck, Nicholas B. CURRENT PRIJON NUMBER: 60/448,797 PRIOR FILING DATE: 2003-02-20 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 4.0 SEATURE: LENGTH: 2073 TYPE: DNA COGANISM: Bacillus thuringiensis FEATURE: NAMEKEY: CDS LOCATION: (1) (2073) US-10-781-979-4
CCATTGCAGNTTTTTATATATATATATATATAGAGGTAGCCGATAGTTTTTTTATAGTCGTTTTATAGTCGTAAAAATTATAGAGGGTATTTTTTATAGTCGTAAAAATTATAGAGGGTATTTTTTATAGTCGTAAAAATTATAGAGGGTATTTTTATAGTCGTAAAAATTATAGAGGGTAATTATTTAT				· : : :
	1 TCTATATGTGATTTATTATTATCTATAATTCGTAAAGGGTAGCCGATAGTGTTTTAAGTGAT 8 GCGATTGCAGATTTTGACGGTAAATTGAAAAATTATAGAGAGTATTATCTTTCTT	TCAAGAACAATGCTCAAGTATTGTTATTACCTACTTTTGCACAAGCTGCAAATGTGCAG TTATTACTATTAAGGGATGCAGTTCAATATAAAGCACAATGGTTCCCATTTTTGAGTGCA TTATTACTATTAAGGGATGCAGTTCAATATAAAGCACAATGGTTCCCATTTTTTGAGTGCA GAGAATGTAAGGAATCGGAATTAATATCACCTAACAGTGGTTGTGGTTTTTACCGGTGATTAC GAGAATGTAAGATCGGAATTAATATCACCTAACAGTGGTTGTGTTTTTACCGGTGATTAC TATTAAAATGCAAATAATAATCACCTAACAGTGGTTGTGTTTTTACCGGTGATTAC TATTAAAATGCAAAAGGGCAGAGTATACACTTATTGTTTATTGTTACCGTGATTAC TATGAGCGATTAAAATGCAAAAGGGCAGAGTATACAATTAGTTTATTGTTTATTGTTATTGTTTCAC TATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTTGTTTATTGTTTTCAC TATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTTGTTTTTTTT	GTAGGTTTAAATCAGATAAAACAGGGGGCAGGTGCTGACACTTGGTCGAAATTTAAT	GCGTTAGAGGCTAATGGAACACGGGACCTGGTTTAGTTACTTGGCTTAGCAAATAGGT GCGTTAGAGGGCTAATGGAACACGGGGACCTGGTTTAGTTACTTGGCTTAGCAAATAGGT ATATAATGAGGAACACGGGGACCTGGTTTAGTTACTTGGCTTAGCAAATAGGT ATATATAATGAGTATGTTTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAA ATATATAATATGAGTATGTTTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAA ATATATATATATAATGAGGTATTTTTCAACGTATGTCTGGGAACTCGTCATTATATATA

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                                              APPLICANT: Graczi, Nadine
APPLICANT: Graczi, Nadine
APPLICANT: Graczi, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Brian
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274147
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,797
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 66.
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28.2%; Score 1686; Di
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches
       S-10-781-979-6
Sequence 6, Application US/10781979
Publication No. US20040250311A1
GENERAL INFORMATION:
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NAME/KEY: CDS
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Sequence 4, Application US/10929754
Publication No. US20050124803A1
GENERAL INFORMATION:
APPLICANT: ABDULLAH, MODH AMIR
APPLICANT: DEAN, DONALD H.
TITLE OP INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
FILE REFERENCE: 22727/04179
CURRENT APPLICATION NUMBER: US/10/929,754
CURRENT FILING DATE: 2004-08-30
PRIOR PILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 43
SOPTWARE: Patentin Ver. 3.2
SEQ ID NO.
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Pred. No. 2.2e-192;
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Best Local Similarity 74.8%;
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                                                                   APPLICANT: Carcati, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Machael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Brian
ITILE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
ITILE OF INVENTION: AXMI-014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 855; DB 8; Length 21
Pred. No. 5.5e-169;
0; Mismatches 430; Indels
               Sequence 1, Application US/10782141 Publication No. US20040197917A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 1255; Conservative
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3072 GATTCCATATGTTACAATGATTGGTTGTCAGATGTTCCAGGTATGAATTATGATATCTA 3131
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                                                                                     2772 TACAAATGAAATATAGGGGTTTGGGTCATGTTTAAAATATCTTCTCCAGATGGATACGC
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Publication No. US20040197917A1

GENERAL INFORMATION:

APPLICANT: Garozzi, Nadine

APPLICANT: Hargiss, Tracy

APPLICANT: Margiel, Michael G.

APPLICANT: Carr, Brian

APPLICANT: Carr, Brian

TITLE OF INVENTION: AXML-014, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for Its Use

FILE REFERENCE: 045600/274143
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Pred. No. 5.4e-155;
0; Mismatches 415; Indels
                                                                            Sequence 2, Application US/10929754
Publication No. US20050124803A1
GENERAL INFORMATION:
APPLICANT: ABDULAH, MODH AMIR
APPLICANT: BEAN, DONALD H.
TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHIPTION:
TILLE OF INVENTION: LOS 22727/04179
CURRENT FILING DATE: 2020-408-30
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Bacillus thuringiensis
 ACGTCACAGCTGGGCCT 1710
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Best Local Similarity 71.3%;
Matches 1092; Conservative C
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US-10-929-754-2
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             736 AAGGGTTTAGATCAGATAAGACAGGCGGGTACAAGTGCTGAAGTTTGGTCGAAATTTAAT 795
                                                      AAATTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACTTAT
                                                                                                                                                                     1536 AGGATGACAATTGAATCTACGTTCCCACTTGT-----ATTGCACTCTAATGGTGTTAGA
                                                                                   AAATTTCGTAGAGAAATGACGTTCGCGGTATTGGATATTATTGCTATATTCCCAACTTAT
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                                                                                                                                                                                                                                                                 916 CCAGTGGGATATTCAGGGGGAAATTATGGTTGGGAACGGTTTT-----TTAGCTTTAAT
                                                                                                                                                                                                                                                                                                                 GGGTTAGAGGCTAATGGAACACGGGGACCTGGTTTAGTTACTTAGCTTAGCAAAATAGGT
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                                                                                                                                          GATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT
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PUblication No. US20040197917A1

GENERAL INFORMATION:

APPLICANT: Carozii, Nadine

APPLICANT: Koziai, Michael G.

APPLICANT: Koziai, Michael G.

APPLICANT: Carr, Nicholas B.

TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for Its Use

TITLE OF INVENTION: Methods for Its Use

TITLE OF STATE OF ST
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US-10-782-141-4
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Pred. No. 2.5e-146;
0; Mismatches 423; Indels
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR PILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 2019
                                                                                                                                                                                TYPE: DNA ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.8%;
Matches 1143; Conservative 0
                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-10-782-141-2
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1447 IGGACACATACAAGTATGAAAAAGATAATCGAATTTATCCAGATAAAATTAGGCAAATT 1506
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                      AGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAG
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                                          AGAGAAATGACGTTGGCGGTATTGGATATTTGCTATATTTCCAACTTATGATTTTGAA
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Publication No. US20020182693A1

GENERAL INPORMATION:
APPLICANT: TANARA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: HASEGAWA, Makoto
APPLICANT: ETARA, Gaku
APPLICANT: KIMURA, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: KISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: poynucleotide encoding the same
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US-10-120-544A-3
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Pred. No. 8.9e-145;
0; Mismatches 422;
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 600448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
LENGTH: 2010
                                                                                                                                 ONGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.7%;
Matches 1135; Conservative
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US-10-782-141-4
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APPLICANT: TANAKA, Masao

APPLICANT: TANAKA, Tomoko

APPLICANT: ACYGI, Moriichi

APPLICANT: ACYGI, Moriichi

APPLICANT: BHASEGAWA, Makoto

APPLICANT: BHASEGAWA, Makoto

APPLICANT: BHASEGAWA, Makoto

APPLICANT: KIMUKA, Masaharu

APPLICANT: KIMUKA, Masaharu

APPLICANT: NISHIHASHI, Hideji

TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and

TITLE OF INVENTION: poynucleotide encoding the same

TITLE OF INVENTION: Doynucleotide encoding the same

TITLE OF ILING DATE: 2005-03-29

CURRENT APPLICATION NUMBER: UP 2001-115754

PRIOR FILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0
                                 GTTACGCAAGCTTAGATGATTTGGAAGTGATTGAAGAAGAGGCGCTGGGTGTCGAAGCAT
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LENGTH: 4359
TYPE: DNA
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                                                                                                                                                                                                                                                                                                         Score 390; DB 5; Length 4359;
Pred. No. 4.6e-71;
0; Mismatches 535; Indels 5
CURRENT APPLICATION NUMBER: US/10/120,544A;
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
NUMBER: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH. 4359
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.0%;
Matches 815; Conservative 0
                                                                                                                                                                                           ORGANISM: Bacillus popilliae
                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-10-120-544A-3
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Sequence 2, Application US/10089678

Sequence 2, Application US/10089678

Publication No. US20030017967A1

Publication No. US20030017967A1

APPLICANT: ASANO, Shinichiro

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/089,678

CURRENT FILING DATE: 2002-08-03

PRIOR PAPLICATION NUMBER: PC1/JP01/06660

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 3

SOGTWARE: Patentin version 3.1

SEQ ID NO 2
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                             - TGAACAAGAGTTACACTATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGG
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                                                                                                                              TACAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATG
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                                                                                                                                                                                                       54;
                                                                                                                                                         Length 4359;
                                                                                                                                                                                                            Indels
                                                                                                                                                      Score 390; DB 10;
Pred. No. 4.6e-71;
0; Mismatches 535;
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Best Local Similarity 58.0%;
Matches 815; Conservative C
popilliae
                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-654-3
ORGANISM: Bacillus
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Sequence 3, Application US/10089678

Publication No. US20030017967A1

GENERAL INFORMATION:

TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,

TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

CURRENT APPLICATION NUMBER: US/10/089,678

CURRENT APPLICATION NUMBER: US/200-236140

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO
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                                                                                    2401 TATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAACTGGC
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              TGTAACGATGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGCGAAGA
                                                                  GATATATGACAAAACAGTAGAGGTATT
                                                                                            3540 TGATACAGGTGTTTTATCTGCTGATCAACTAGCTATATCACAAAAACAGTGGAATTCAC
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Pred. No. 4.8e-56;
0; Mismatches 519;
                                                                                                                                                                            3733 TAGCATCGAGTTGCTTTGTATGCAAGGATA 3762
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Best Local Similarity 55.7°
Matches 831; Conservative
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                                                            3573 GTTATGTATTGCGTGTCACGGCGAGAAAAGAAGATCCGGGAGCTGGCAATGTTACCTTA 3632
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                                                                                                                                                                                                                              Sequence 19, Application US/11091654

Publication No. US2005017235A1

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APPLICANT: KIMURA, Masaharu

APPLICANT: NISHIHASHI, Hideji

TITLE OF INVENTION: poynucleotide encoding the same

TITLE OF INVENTION: poynucleotide encoding the same

TITLE OF INVENTION: poynucleotide encoding the same

FILE REFRENCE: OP1335

CURRENT FILING DATE: 2001-01-15754

PRIOR FILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SEOFWARE: Patentin Ver. 2.0

SEOFWARE: Patentin Ver. 2.0
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                                                                                                                          3633 GTGACTGTGAAATCATGTCGACAAGCTGAGCTTTACTTCTTGCGATATAG 3683
                                                                                                      3594 TGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGCGAAGAAG
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ORGANISM: Bacillus popilliae
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2433 AGGAGAATCCATGGAAAACAAGTCCGAATGTTACGATCCGACAAGATAACCCGATTTTTA 2492
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Search completed: December 20, 2005, 04:49:14 Job time: 2972.36 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 3, Application US/11091643
; Sequence 3, Application US/11091643
; Publication No. US2050246789A1
; GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
; APPLICANT: TOXOXAMA, TOMOKO
; APPLICANT: ANGEGAMA, Makoto
; APPLICANT: HASEGAMA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: EHARA, Gaku
; APPLICANT: EHARA, Gaku
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: Polypeptide encoding the same
; TITLE OF INVENTION: Polypeptide encoding the same
; TITLE OF INVENTION: POLYBER US/11/091,643
; TITLE OF INVENTION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver: 2.0
; SSOFTWARE: Patentin Ver: 2.0
; SSOFTWARE: Patentin Ver: 2.0
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            US-11-108-389-59
US-11-108-389-59
US-11-108-389-89
US-11-108-389-91
US-11-058-727-21
US-11-058-727-22
US-11-058-727-23
US-11-058-727-49
US-11-058-727-67
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US-11-058-727-67
US-11-068-727-67
US-11-108-389-21
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ORGANISM: Bacillus popilliae
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-643-3
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Sequence 57,
Sequence 59,
Sequence 89,
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| Cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/NS10_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-091-643-19
US-11-091-643-17
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US-11-08-727-1
US-11-08-727-1
US-11-08-727-17
US-11-08-389-17
US-11-08-389-18
US-11-08-389-18
US-11-070-575-4
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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Result No.

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                                                                                                AAGAAGGACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGGCAGGAAACAC 3620
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: YONGYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
APPLICANT: AOYAGI, Moriichi
APPLICANT: HASEGAWA, Makocto
APPLICANT: EHARA, Gaku
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHABHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: polypeptide having the same
TITLE OF INVENTION: 2001-0130
TITLE OF INVENTION: 2005-03-29
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,643
CURRENT PILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR PLICATION NUMBER: JP 2001-115754
PRIOR PLICATION NUMBER: JP 2001-115754
PRIOR PLICATION NUMBER: JP 2001-03463
PRIOR SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                           TGTCGCAAGATCTTTGTATCGAACACAATCGCGGTTATGTATTGCGTGTCACGCGAGAA
                                                                                                                                AAGAAGATCCGGGAGCTGGCAATGTTACCTTCAGTGACTGTGCAAACCATGTCGACAAGC
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                                 TATCTCAAAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAA
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Pred. No. 3.8e-58;
0; Mismatches 519;
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US-11-091-643-19
'Sequence 19, Application US/11091643
'Publication No. US20050246789A1
'GENERAL INFORMATION:
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il Similarity 55.7%;
831; Conservative
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ORGANISM: Bacillus popilliae
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Best Local Similarity
Matches 831; Conserv
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; LOCATION: (224)
US-11-091-643-19
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APPLICANT: YOKOYAMA, TOMOKO
APPLICANT: YOKOYAMA, TOMOKO
APPLICANT: ANGRAI, Moriichi
APPLICANT: ANGRANA, Makoto
APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Masaharu
APPLICANT: HASEGAWA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: Doynucleotide encoding the same
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,643
CURRENT FILING DATE: 2005-03-29
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
SOFTWARE: PATCATION NUMBER: UP 2001-15754
SPIOR SEQ ID NOS: 22
SOFTWARE: PATCATION SEC 22.0
SOFTWARE: PATCATION OF 2.0
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Pred. No. 6e-56;
0; Mismatches 533;
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                           Sequence 5, Application US/11091643
Publication No. US20050246789A1
GENERAL INFORMATION:
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                                                                                                APPLICANT: TANAKA, MASAO
APPLICANT: YOKOYAMA, TOMOKO
APPLICANT: AOYAGI, Moriichi
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Best Local Similarity 55.2
Matches 817; Conservative
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; LOCATION: (1)..(4158)
US-11-091-643-5
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APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James F. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PastSEQ for Windows Version 4.0
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ORGANISM: Bacillus thuringiensis
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; OTHER INFORMATION: Cry1218-1
US-11-058-727-1
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FEATURE:
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                                             GIGAATTIGATCGATGCAAGCCCTATTCGTATCCACCTTTACTTCCAGAATGTAACCCTG 2662
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APPLICANT: Andre R. Abad; APPLICANT: Ronald D. Flannagan; APPLICANT: Rafael Herrmann; APPLICANT: Theodore W. Kahn
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CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-05
PRIOR PILING DATE: 2003-06-25
PRIOR PILING DATE: 2003-06-25
SROFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                 ORGANISM: Bacillus thuringiensis
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| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (0)...(0)
| OTHER INFORMATION: CFy1218-1
| US-11-108-389-1
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APPLICANT: Ronald D. Flannagan
APPLICANT: Refael Herrmann
APPLICANT: Thecotore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
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Publication No. US20050261188A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        DB 7; Length 3633
                                                                                                                                                                                                                                                                                      Query Match 5.1%; Score 307; DB 7; Length 36: Best Local Similarity 55.7%; Pred. No. 1e-55; Matches 763; Conservative 0; Mismatches 530; Indels
                  LENGTH: 3633
TYPE: DNA
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                           ; LOCATION: (0) ... (0)
; OTHER INFORMATION: Cry1218-2
US-11-058-727-3
                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3633)
FEATURE:
NAME/KEY: misc_feature
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                TCTTATTAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAAGTCATTG
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APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Balbert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James F. H. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
PRIOR PRILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-66-25
PRIOR PRILING DATE: 2003-66-25
PRIOR FILING DATE: 2003-66-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050261483A1
GENERAL INFORMATION:
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                                                                                               Score 307;
Pred. No. 1
                                                                                               5.1%;
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-2
US-11-108-389-3
                                                                                               Query Match
Best Local Similarity 55.77
Matches 763; Conservative
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APPLICANT: Ronald D. Flannagan
APPLICANT: Refael Herrmann
APPLICANT: Refael Herrmann
APPLICANT: Refael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: James F.H. Wong
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APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANTON: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT FILING DATE: 2005-04-18
FRIOR APPLICATION NUMBER: 60/491,786
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 10/606,320
FRIOR FILING DATE: 2003-04-04
FRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
CONTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
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OKGANISM: Bacillus thuringiensis
PEATURE:
NAME/KEY: CDS
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LENGTH: 3633
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        CAGGCGTAACGGATTATGAAGTGAATCAAGCGGCAAACTTAGTGGAATGCCTATCGGATG
                                                                                                                       AACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTA
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55.7%; Pred. No. 1.1e-55;
iive 0; Mismatches 530; Indels 76
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APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: Go-Guo. Yu
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: 05/391,786
PRIOR PELLING DATE: 2005-02-15
PRIOR PILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-06-26
PRIOR PILING DATE: 2003-06-26
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PASTSE
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; OTHER INFORMATION: Genomic DNA 1218-1
US-11-058-727-17
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Publication No. US20050261483A1
GENERAL INFORMATION:
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                                                                                                                                  GATATGTGTTACGTGTGATTGCCAAAAAAAAGAGGACCTGGAAAAGGGTATGTAACGATGA 3593
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Publication No. US200S0261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theedore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
FILE REFERRACE: 35718/291049
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/361,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR SPLING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
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                                                                    3700 scasicaasarissaaarricacaarrosica---
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APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan; APPLICANT: Rafael Herrmann
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: Gao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING OBTE: 2003-04-04
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LOCATION: (0)...(0)
OTHER INFORMATION: Genomic Cry1218-2
                                                                                                                                                                            Sequence 18, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
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ATATGTATGCATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCACGATCGTCATC 2939
                                          3833 grarigranakgccgrrragaagragaaakcgrrcrgcrgaagcg------carg 3882
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Publication No. US20050271642A1
GENERAL INFORMATION:
APPLICANT: ASANO, Shin-ichiro
APPLICANT: ADAMA, Mikiko
APPLICANT: BANDO, Hisanozia
TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
FILE REFERENCE: 59562200300
CURRENT FILING DATE: 2005-03-01
PRIOR PLILING DATE: 2005-03-01
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 4119
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          APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPRENCE: 35748/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2005-04-18
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
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, OTHER INFORMATION: Genomic Cry1218-2
US-11-108-389-18
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Sequence 1, Application US/11091643

Publication No. US2060246789A1

GENERAL INFORMATION:

APPLICANT: TANAKA, Masao

APPLICANT: YOKYAMA, TOMOKO

APPLICANT: WISHIMASHI, Marichi

APPLICANT: EHARSEAWA, Makoo

APPLICANT: EHARSHI, Hideji

TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

TITLE OF INVENTION: Polypeptide encoding the same

TITLE OF INVENTION: popunclectide encoding the same

TITLE OF INVENTION: popunclectide encoding the same

TITLE OF INVENTION: UNBER: JP 2001-115754

PRIOR FILING DATE: 2001-04-43

CURRENT FILING DATE: 2001-04-43

PRIOR FILING DATE: 2001-04-43

PRIOR FILING DATE: 2001-07-44

PRIOR SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                   TATTTACAAA-----TGAACAAGAGTTACACTATCATATTACTTTAGATCATATTCAAA
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2.6%; Score 152.8; DB 9;
Best Local Similarity 63.2%; Pred. No. 2.1e-23;
Matches 254; Conservative 0; Mismatches 142;
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; LOCATION: (1)..(402)
US-11-091-643-1
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                                                                                                                                                                         2292 AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGGAACAAAAATACGTTAAAAA
                                                                                                                                                                                                                                                               2412 AACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTA
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                                                                                                                                  Gaps
                                                                         Query Match 5.0%; Score 301; DB 7; Length 4119; Best Local Similarity 55.4%; Pred. No. 2e-54; Matches 819; Conservative 0; Mismatches 530; Indels 130;
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; ORGANISM: Bacillus popilliae
US-11-070-575-4
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                                                                                615 GTATGAAACTGGTTTAGCAAATTAAAA-----GGCACGAGCGCTAAACAATGGGTTGA 668
 729 AAATTATGACACGCACGTACCCAATGGAAACGAAAGCACAACTAACAAGGGAAGTATA 788
                                                                                                                  1001 ATTTAATAAATTTGGTAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC
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1.5%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 2.4e-09;
Matches 171; Conservative 0; Mismatches 112; Indels 6
                                                                                                                                                                                                                                                                                                                                                                               CAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCT 3304
                                                                                                                                                                                                                                                                                                                                                                                                  361 CAGTCGATTCCTTATGTATATAATAATATGTACCGGAAGTT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus thuringiensis (truncated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/11058727; Publication No. US20050261483A1; GENERAL INFORMATION:
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COTHER INFORMATION: 49PVD
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LOCATION: (10)...(1860)
FEATURE:
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Pred. No. 2.2e-161;
                      US-09-668-650-9

US-09-688-671-1

US-09-589-477-71

US-09-589-2858-71

US-09-581-32A-39

US-08-179-6588-4

US-08-179-6588-4

US-08-179-6588-4

US-09-119-809-4

US-09-11-177-4

US-09-220-806-4

US-09-220-806-4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09224024 Patent No. 6056953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 504-372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3543 base pairs
TYPE: nucleic acid
strandEdness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%;
71.5%;
                               Query Match
Best Local Similarity
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APPLICANT: City: San Diego
APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030
APPLICANT: Telex number: (199) 453-8030
APPLICANT: Telex number: TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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STREET: 2421 N.W. 416t Street, Suite A-1
CITY: Gainesville
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Veri
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US94/07902
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NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3543 base pairs
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STRANDEDNESS: single
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CLASSIFICATION:
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Sequence 2, Application US/10089678

Sequence 2, Application US/10089678

Patent No. 6952977

GENERAL INFORMATION:

APPLICATOR: ASANO, Shinichiro

ITILE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,

ITILE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

FILE REPERBURE: 068821

CURRENT APPLICATION NUMBER: US/10/089,678

CURRENT APPLICATION NUMBER: US/10/089,678

PRIOR APPLICATION NUMBER: PCT/JP01/06660

PRIOR APPLICATION NUMBER: PCT/JP01/06660

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 3504
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     3320 TCTTACGTGTTATTGCCAAAAAGGAAGGACCTGGAAATGGGTATGTCACGCTTATGGATT
                                                           ATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTT
                                                                                        ATGTTCCAGGTATGAATTATGATATCTATGTAGAGTTGGATGCACGAGTGGCACAAGCGC
                                                                                                                                    ATAATTTATATGAGGACGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGG
                                                                                                                                                                 3140 GTTATTTGTATGATACAAGAAATATTATAAAATGGTGATTTTACACAAGGGGTAATGG
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US-10-089-678-2
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                                                                                                                                                                                  AAACAGTACAACAATAATTAATACATTTTATGCAAATCCTATAAAAAACACTTTACAAT
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                                                                                                                 Gaps
                                                                                                                 24;
                                                                          Length 3543;
                                                                                                               Indels
                                                                        Score 765.8; DB 6;
Pred. No. 2.2e-161;
0; Mismatches 397;
                       (genomic)
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Best Local Similarity 71.5%;
Matches 1058; Conservative
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TOPOLOGY: linear
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ORGANISM: Bacillus thuringiensis
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Best Local Similarity 55.4
Matches 881; Conservative
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2193 GAAACGACTTGTTCAGGCACGTAACTTACTCCAAGATACAGGCTTTAATAGGATTAATGG
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                        TACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAATG
                                                2073 TGCCTTACAGACAAGTGTAACGGATTATCAAGTGAATCAAGCGGCAAACTTAGTAGAATG
                                                                                             2133 CCTATCCGATGAGTTATACCCAAATGAAAACGAATGTTATGGGATGCAGTGAAAAAGGGC
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RESULT 4

US-10-089-678-3

is Sequence 3, Application US/10089678

is Patent No. 6562977

GENERAL INFORMATION:

APPLICANT: ASANO, Shinichiro

ITILE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, PRILE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, PRILE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, PRILE OF INVENTION NOWBER: US/10/089,678

CURRENT APPLICATION NUMBER: US/200-204-03

PRIOR PELING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN VERBION 3.1

SEQ ID NO 3

SEQ ID NO 3

TENTING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 3
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                                                    3114 ICGAAATGGATTAAGTGATTGGAATGCAACATCAGATGTGAATGTGCAACAACTAAGCGA
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3420 ACCGAATTATAGATATGTGTTACGTGTCACAGAGAAAAAAGAGGAGTAGGAAGAACGATA 3479
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                                                                           TGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGCGAAGA
                                                                                                           APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTON: No. 5359048el Microorganism and Insecticide
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                3733 TAGCATCGAGTTGCTTTGTATGCAAGGATA 3762
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obba, Michio
Iwahana, Hidenori
Sato, Relichi
Suzuki, No. 5359048ukazu
Ogiwara, Katsutoshi
Sakanaka, Kazunobu
Hori, Hidetaki
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MEDIUM TYPE: RIOPY disk
COMPUTER: RIOPY disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,203
FILING DATE: 19920723
CLASSIPTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REESCOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEPHONE: 904-375-9100
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STRAIN: japonensis
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ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3797 base pairs
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STRANDEDNESS: single
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FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
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                                                                                                                                                                                                                                                                                   TATCTGTCAAAAATTAGATGAGTCTAAATTAAAACCATATACACGTTATCGAGTAAGAGG
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2461 AAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGAT--
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                                                                                          2519 -----TGGACATTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTAA
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3299 AATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTAAAGGCACGTATCATGCAAGGT 3358
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                                                                                  3175 GAAATCCCTGGAATGAACTATACGAGTTTACAGAGTTAACAAATAGACTCCAACAAGCA
                                                                                                                                            3359 TATAATTTATATGATGCACGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAG
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APPLICANT: Sato, Relichi
APPLICANT: Sato, Relichi
APPLICANT: Sato, Relichi
APPLICANT: Satoni, No. 5747450ukazu
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Hori, Hidetaki
APPLICANT: Hori, Hidetaki
APPLICANT: Asano, Shouji
APPLICANT: Kawaugi, Tadaaki
APPLICANT: Kawaugi, Tadaaki
APPLICANT: Rawaugi, Tadaaki
APPLICANT: Rawaugi, Tadaski
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APPLICANT: Rawaugi, Tadaski
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,887
FILING DATE: 00-000-1994
CLASSIFICATION: 800
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REGISTRATION NUMBER: 31,794
REGISTRAC/DOCKET NUMBER: M/K 301
TRLECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: David R. Saliwanchik : 2421 N.W. 41st Street, 8 Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08272887
Patent No. 5747450
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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US-08-272-887-1
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                                                                                                                  Gaps
                                                                                                                  603
                                                          Length 3797;
                                                       Query Match 6.0%; Score 358; DB 2; Length 37; Best Local Similarity 56.8%; Pred. No. 3.4e-70; Matches 776; Conservative 0; Mismatches 530; Indels
US-07-915-203-1
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GATGCATTATTTACAAATGAACAAGAGTTACACTATCATATTACTTTAGA-----TCAT 3238
                                                                                       GATCGTTTATTCGCAGATTATCAAGACCAAAACTTAATTCTGGTGTAGAAATGTCAGAT 3114
                                                                                                                                             3239 ATTCAAAACGCTGATCGACTGGTACAGTCGATTCCCTATGTATACCATAATTGGTTACCG 3298
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    3235 TGGAATTTGTATGATCTTCAAAACGCTATACCAAATGGAGATTTTCGAAATGGATTAAGT 3294
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APPLICANT: Obba, Michio
APPLICANT: Sato, Relichi
APPLICANT: Sato, Relichi
APPLICANT: Suzuki, No. 5824878ukazu
APPLICANT: Suzuki, No. 5824878ukazu
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Hori, Hideraki
APPLICANT: Asano, Shouji
APPLICANT: Asano, Shouji
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,449
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,887
FILING DATE: 08-JUL-1994
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08789449 Patent No. 5824878
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COUNTRY: US
ZIP: 32606
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US-08-789-449-1
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                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                           Length 3797;
                                                                                                                                                                                                                                                      Query Match
6.0%; Score 358; DB 2; Length 379°
Best Local Similarity 56.8%; Pred. No. 3.4e-70;
Matches 776; Conservative 0; Mismatches 530; Indels
                                                               Bacillus thuringiensis
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                                                                                          STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibui
                        DNA (genomic)
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187..3636
linear
                     MOLECULE TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-272-887-1
TOPOLOGY:
                                                               ORGANISM:
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                                       TTAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAA 3064
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Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                          GGACCACTAACAGGTGAAGCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAAACAA
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STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
APPLICATION UNDER: US/07/876,280
FILING DATE: 19920430
CLASSIPICATION: 514
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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US-07-876-280-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2297 GCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTACGAAAAATACGTTAAAAATAGAA 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2374 GCACGTAACTTACTCCAAGATACAGGCTTTAATAGGATTAATGGAGAAAACGGATGGACG 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2314 TACCCAAATGAAAAACGAATGTTATGGGATGCAGTGAAAGAGGGGAAACGACTTGTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2525 TTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2434 GGAAGTÁCGÁGAÁTCGAGGTTÓTGGAAGGAGÁTGTTCTGTTTÁAÁGATCGTTCGCTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2585 ATGCGTGGAGCACGAGACATATAGGAACTCTATTTCCAACCTATATCTGTCAAAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAGTCTAAATTAAAACCATATACACGTTATCGAGTAAGAGGGTTTGTGGGGAAGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2197 GCAAAGAAAGCTGTGAATGGCTTGTTTAC---GAATGAAAAAAAGATGCCTTACAGACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2254 GTAACGGATTATCAAGTCAATCAAGCGGCAAACTTAATAGAATGCCTATCCGATGAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2477 TCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGAT-----TGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2674 GATAATCTCTTGCCAGATGTACGCCCTGTCAATTCTTGTGGTGGAGTCGATCGCTGCAGT
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NAME: Saliwanchik, Davia ...
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOWNUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-375-8100
TELEPAX: 904-375-8100
TELEPAX: 904-375-8100
SEQUENCE CHARACTERISTICS:
LENGTH: 3797 base pairs
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibui
                                                                                                                                                                                                                  LENGTH: 3797 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-789-449-1
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
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Sequence 1, Application US/07812180A
Patent No. 5366892
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
APPLICANT: Sieck, August J
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a
TITLE OF INVENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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         AGTTCTCGCTCCCTATCGATATAGGAGAGCTGGATTACAATGAAAATGCAGGAATATGGG
                                                                                    TIGENTIABBATTACGGACCCAGAGGGATACGCAACACTTGGAAATCTTGAATTAGTCG
                                                                                                                                                                               AAGAGGGACCTTTGTCAGGAGGCGCATTAGAGCGCTTGCAAAGAGAAGAACAACAGTGGA
                                                                                                                                                                                                                   AACAACACATGGAGAAAAAACGTTGGGAAACACAACAAGCCTATGATCCAGCAAAACAGG
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                                                                                                                                                                                                                                                                                                                                                                       -TCATATTCAAAACGCTGATCGACTGGTACAGTCGCTATGTATACCATAATTGGT
                                                                                                                                          AAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGA
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US-07-812-180A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTACCAGATGATTTATTGCCA-------GATGTATCTCCTGTA 2526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACACAACAGATGGATATGCTCCCG 2879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2372 AAGTAGAGGAAGGTGTATTAAAACCATACACAAGATATAGACTGAGAGGGGTTTGTGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACATTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTAAAGGAAAATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.3%; Score 314.6; DB 2; Length 3471; Best Local Similarity 55.7%; Pred. No. 1.7e-60; Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                       STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: E. COli NM522 (pMYC2320) NRRL B-18769
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEFAX: 904-372-5800
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2581 TTAGAAGGAGAAAACCGT----
                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-876-280-29
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ADDRESSEE: Roman Sallwill
STREET: 2421 N.W. 41st Street, Ste A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER: READABLE FORM:
MEDUTER: BM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 1992002
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55.7%; Pred. No. 1.7e-60;
tive 0; Mismatches 559;
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LIBRARY: FONCERRADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus thuringiensis
STRAIN: Kumamotoensis
INDIVIDUAL ISOLATE: PS50C
                                                                                                                                                                                                                                                        FILING DATE: 19920102
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
TELECOMMUNICATION INFORMATION:
TELEFROM: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 DASE PAIRS
TYPE: NUCLEIC AGID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SBRNE: NO
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Matches 838; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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                                                                                                                                                                                                                                                                                  for Controlling Scarab Pests
cillus thuringiensis Isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-04N-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/808,430
FRIOR APPLICATION NUMBER: 07/808,136
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Best Local Similarity 55.7%; Pred. No. 1.7e-60;
Matches 838; Conservative 0; Mismatches 559;
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LIBRARY: FONCERRADA
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
STATE: Gainesville
STATE: FL
COUNTRY: USA
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REGISTRATION NUMBER: 31,794
REFRENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8800
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                                                                                                                                                                                                                    APPLICANT: Foncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Co
TITLE OF INVENTION: with Bacillus
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                               APPLICANT: Michaels, Tracy Ellis
                                                                                                     Sequence 1, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WEDITTER: IBM PC COMPALIBLE
POTATIONS/MS.
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SEQUEBNCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                               Score 314.6; DB 3; Length 3471;
Pred. No. 1.7e-60;
0; Mismatches 559; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCAGTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGG-
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
INMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1638), NRRL B-18751
                                                                                                                                                                                                                                                                                                                                                                   5.3%;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.7°
Matches 838; Conservative
                                                                                                                                                                                                                                                                                        US-07-941-650A-1
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                                            TAGTICTATCAAATTGGAGCGCGGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATG 3533
                                                                                                                                                                                                                                                      3215 GATATGTATTACGAGTTACTGCAAGAAAAGAAGGGGTAGGAAATGGATATGTAAGTATTC 3274
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                                                                                                        3155 TTGTGATTCCAACTGGGATGAACAAGTTTCACAACAGTTTACAGTTCAACCGAATCAA 3214
                                                                                                                                                                                       GATATGTGTTACGTGTGATTGCCAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGA
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GENERAL 10. 6794184
GENERAL INFORMATION:
APPLICANT: Uyeda, Kendrick A.
APPLICANT: Uyeda, Kendrick A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CTTY: Gainesville
STATE: PL
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
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COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 12-8EP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-8EP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,335
FILING DATE: 21-FEB-1991
PRIOR APPLICATION NUMBER: US 07/642,112
PRIOR APPLICATION NUMBER: US 07/642,112
ATCHING DATE: 16-JAN-1991
ATCHING DATE: 16-JAN-1991
ATCHING DATE: 16-JAN-1991
ATCHING DATE: 16-JAN-1991
ATCHING DATE: 16-JAN-1991
ATCHING DATE: DAVICH R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
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1037 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AATAGGCGATGCAGCAAAAGAAGCAGTATCTATTGGGACAAACCATAGTCTCTCTTTATCAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 TCCGACTAATCGTCAAACTGTGTGAGCACTTTCTATATGTGATTTATTATCTATAATTCG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTATTGA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAAATTGAA 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       693 AGAGCTTATT-----GAACT 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 ACCTICITITIGEGAGGGCTGCATTITICCATITATIACTACTAAGGGATGCTACTAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857 TAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2%; Score 308.2; DB 3; Best Local Similarity 48.0%; Pred. No. 4.6e-59; Matches 1607; Conservative 0; Mismatches 1588;
                                                                                                   130-4080/PCT/CIP
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4
TELECOMUNICATION INFORMATION:
TELECHONIS: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     1..3726
                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-001-982-11
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                                                                                                                -TCATATTCAAAACGCTGATCGACTGGTACAGTCGATTCCCTATGTATACCATAATTGGT
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                     CTGTAGATGCATTATTACAAATGAACAAGAGTTACACTATCATATTACTTTAGA-
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APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6204246artis Corporation
STREET: 3044 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09001982; Patent No. 6204246; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                        153 AATAGGCGATGCAGCAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTCTTATCAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                        213 AGCACCTTCTCTTACTGGATTAATTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AGGTAGTAGTAGAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTATTGA 332
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        Indels 156;
                                                                                                                                                                             Length 3726;
                                                                                                                                                                       Score 308.2; DB 3;
Pred. No. 4.6e-59;
0; Mismatches 1588;
                                                                        LOCATION: 1.3726
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                             5.2%;
                                                                                                                                                                                               Best Local Similarity 48.0
Matches 1607; Conservative
MOLECULE TYPE: CDNA
                                                   NAME/KEY: CDS
                                                                                                                         US-09-668-650-11
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                  3237 ATATICAAAACGCIGAICGACIGGIACAGICGAITCCCIAIGIAIACCAIAAITGGIIAC 3296
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                                                                                                                 3297 CGAATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: THE PC COMPUTER: SOFTWARE: PATENTY PC-DOS/MS-DOS
SOFTWARE: PATENTY NATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CIASSIFICATION NUMBER: US/09/001,982
FILING DATE: <UNKNOWN>
PROLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGIGITMATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09668650
Patent No. 6780408
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
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LENGTH: 3726 base pairs
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INFORMATION FOR SEQ ID NO: 11:
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STRANDEDNESS: single
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2352 TAGARACGACAGATTATGAAATAGAGGCCATTTCTATAGAATGTAGATGTAGATG 2365 CCCAACGACATATTAGAAATAGAGGCCAATTTATAGAATCAGAATGTAGATGTA
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1277 TGCCGCTGCGTACCTACCTAC-ACCRCTTGGTTTTTAATAATAATATATATATATATATATATCACTACTA

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                                           2292 AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA
                                                                                 1940 AAAAAGCACAGAAAGCCGTGAATACCTTGTTTACAGAGGG---AAGAAATGCACTCCAAA
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                                                                                                                                                                                              GCTATATCCTTCGTGTCACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCC 3325
3417 AGGGATGGCACGCAACAGGAAATGCCGCGTACAA---CAAATGGATGGAGCTTCAGTAT 3473
                                     TATGCTGGAACGTGAAAGGTCATGTAGATGTAGAAGAGCAAAACAACCACCGTTCGGTCC 3205
                                                                                                                                                          GATATGTGTTACGTGTGATTGCCAAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGA 3593
                                                                           3474 TAGTICIATCAAATIGGAGCGCGGGGTAICICAAAACTIGCAIGCTCAAGAICAICAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Payne, Jewel M.
APPLICANT: Fu, Jenny M.
TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 305.4; DB 2;
Pred. No. 1.9e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19921106
CLASIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/788,638
FILING DATE: 6-NOV-1991
ATORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERNCE/DOCKET NUMBER: 31,794
REFERNCE/DOCKET NUMBER: MAG8.C1
TELECHMUNICATION:
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APPLICATION NUMBER: US/07/973,320
FILING DATE: 19921106
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ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/07973320
Patent No. 5286486
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HYPOTHETICAL: NO
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INDIVIDUAL ISOLATE: HD867
IMMEDIATE SOURCE:
LIBRARY: Lamdagem (TM)-11
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: F
COUNTRY:
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US-07-973-320-3
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                                                                                                                                                                                                                                                                                                                     Query Match 5.1%; Score 302.2; DB 2; Best Local Similarity 53.5%; Pred. No. 9.9e-58; Matches 807; Conservative 0; Mismatches 618;
                                                                                                                                                                                                                              LIBRARY: Lamdagem (TM)-11 llbrary of J.M. Fu CLONE: 511
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENNE: NO
ORIGINAL SOUNCE:
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                       STRAIN: dakota
INDIVIDUAL ISOLATE: HD511
IMMEDIATE SOURCE:
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APPLICANT: Pu, Jenny M.
TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRIED COUNTRIED COUNTRIED COUNTRIED COMPUTER TRADABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 19921106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19921106
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 0.07/788,638
FILING DATE: 6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET VUMBER: MA68.C1
TELECOMMUNICATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-8100
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Patent No. 5286486
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3414 base pairs
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2678 ATGGCCCAGTTATTGGAGAAGCATTAGCCCGTGTGAAGCGCCCAAGAAACGAAGTGGAGAA 2737
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X58534 B.thuringle X58120 B.thuringle AR359378 Sequence AR359378 Sequence US08188 Bacillus th AB16165 Bacillus AB18105 Bacillus AR315422 Paenibaci CO668322 Sequence CO668322 Sequence CO668318 Sequence AB115422 Paenibaci CO668318 Sequence AR35936 Sequence AR35936 Sequence AR35936 Sequence AXO98657 Sequence AXO98653 Sequence AXO98653 Sequence AXO98653 Sequence AXO98653 Sequence AXO98653 Sequence AXO98653 Sequence AXO98653 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence AXO98659 Sequence	DNA linear PAT 13-SEP-2004 62. Bacillaceae; Bacillus; Bacillus for their use 2004; ngiensis" EYEILESSSNNTNTPNRYPPAANRDMSTMSWND EXTERLESSONTLLSIGKLIPTNSOTYSALSI KLÄNYREYLSYLGAMLKOGREDOGTTNSOTOO OULLLPTPAQAANVQLLLLRDAVQYKAQNFPEL	SABNVRSELISPNSGCOPTGDYYBRIKCKTABYTNYCLYWYQYGLNQIYQGGTGADTW SKENKFRREBATLAVLDIIAI PFTYDFBKYPLPTHVBLTREITDAVQYSGGTYSAULAN WRMTFNGLEANGTRGDELYWHLSKIGIYNBYYBRYFAGWYGTBHYBDYTKGNOIFORN SGTTSNDLRNIDFQNADVYKITSLAIMULVGETTARPEYRVSKADFRRVGGPDLNYDA SGNGLSRWTIESTFPLVLHSNGYRGPSHRLSNAGVYVGNSRVNYYGGTHTSLKRENI TANOITQIPAVKSYYLOWTANAYYTVIKGTHTGGDLIRFLRKSEYNAVYAGGGIR LIINNKYRAGOSYRIRFRYAADKAAFSVYLKGGDLIRFLRKSEYNAVYAGGGIR LIINNKYRAGOSYRIRFRYAADKAAFSVYLYGGGIRGSNRFVSLEKSYSGNYDDLKYSD FKFAEIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLFSNTTTLEYEGERDLEK TKNAVNDLFTN"
168.6 8.1 1837 1 BTCRYIGL 160.6 7.7 2407 6 AR359378 120.6 5.8 2024 1 BTURRYIGL 120.8 5.8 2024 1 BTURRYIGL 120.8 5.8 2024 1 BTURB188 113.6 5.5 3931 1 AB161456 102.4 4.9 16914 1 AB161452 99.6 4.8 1986 6 CQ868322 99.6 4.8 2049 6 CQ868322 99.6 4.8 2049 6 CQ86832 99.5 4.6 4173 6 AX359382 95.5 4.6 4173 6 AX359382 95.5 4.6 4359 6 BDL77493 95.2 4.6 4359 6 BDL77493 95.4 4.5 1959 6 AX098657 93.4 4.5 3684 6 190319 93.4 4.5 3684 6 AX3538 93.4 4.5 3684 6 AX3538 93.4 4.5 3684 6 AX3538 93.4 4.5 3684 6 AX3538 93.4 4.5 3684 6 AX3538	CQ868312 CQ868312 CQ868312 CQ868312. CQ868312. CQ868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG868312.1 CG76883.8 CG87683.1 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76883.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG76888.8 CG768888.8 CG768888.8 CG768888.8 CG7688888.8 CG76888888.8 CG76888888888888888888888888888888888888	SAENVRSELISPNSGOPTGDYYERLKCK SKENKFRERTLAVLDIIAIFPTYDFEKY WPNTFRGLEANGTRGPGLVYHLSKIGIYN SGTTSNDLRNIDFQNADVYKITSLAIMNL GNNGLSRMTIESTFPLVJHSNGVRGPSHR IEANQITQIPAVKSYLQNYLANAYTYVI LIINNKTAGGSYRIRFRYAADKAAFFSYY FKFAEIITPPLPSSNIQMDVEMQANSFQS TKNAVNDLFTN"
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icore version 5.1.6 1993 - 2005 Compugen Ltd. Ing sw model 15, 12:54:35; Search time 6793.75 Seconds (without alignments) 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec 17420.151 Million cell updates/sec	ults predicted by chance to have a the score of the result being printed, the total score distribution. SUMMARIES Description CQ668312 Sequence CQ668314 Sequence AB07414 Bacillus CQ68325 Sequence CQ68324 Sequence CQ68325 Sequence CQ68327 Sequence CQ68327 Sequence CQ68327 Sequence	÷ ;

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RESULT 2 CQ868311 LOCUS LOCUS DEFINITION Sequence 12 from Patent W02004074462. ACCESSION CQ868311, GI:51998357	S Bacillus thuri ISM Bacillus thuri Bacteria; Firm		JOURNAL Patent: WO 2004074462-A 12 02-SEP-2004; Athenix Corporation (US) FEATURES Location/Qualifiers SOURCE 15980	/organism="Bacillus thuringiensis" /mol_type="unassigned DNA" /db_xref="taxon:1428"	Query Match 100.0%; Score 2082; DB 6; Length 5980; Best Local Similarity 100.0%; Pred. No. 0; Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AAAGATGAGTCCATATCAAAATAAAATGAATATGAAATATGGAATCCTCATCG 60	Oy 61 AATAACACAAATACGCCAAACAGATATCCTTTTGCAAATAATCGGGATATGTCTACTATG 120	AAACGATA 		ACACTATTATCAATAATAGGAAAACTAATTCCGACTAATCGTCAAACTGTGTCACCTT	TTAAGTGAT TTAAGTGAT	Oy 361 GCGATTGCAGATTTTGACGGTAAATTGAAAATTATAGAGAGTATTATCTTATCTT 420	TCGGACAA TCGGACAA				661 GAGAATGTAAGATCGGAATTAATATCACCTAACAGTGGTTGTGATTTTACCGGTGATTAC

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1801 TGGGGTTCAAATGTTTTGTATCGCTTGAAAAATCTTACTCTGGAAATTATGAC 1968 TGGGGTTCAAATGTTTTGTATCGCTTGAAAAATCTTACTCTGGAAATTATGAC 1861 AAATATAGTGATTTTAAATTCGCTGAAATTATCACACCTCCATTACCTACGTTCA 2028 AAATATAGTGATTTTAAATTCGCTGAAATTATCACACCTCCATTACCTAGTTCA 2028 AAATATAGTGATTTTAAATTCGCTGAAATTATCAATCACCTCCATTACCTAGTTCA 1921 CAGATGGATGTGGAAGTGCAAGCGAATAGTTTTCAATCAGTGTAAACGTGGTT	Db 2088 CAGATGGATGTGGAGATGGATAGTTTTCAATCAGATGAAAGGGGTTCTCGAC 2147		VERSION CQ868314.4 VERSION CQ868314.1 GI:51998360 KEYWORDS . SOURCE Bacillus thuringiensis ORGANISM Bacillus thuringiensis Bacteria; Firmicutes; Bacillaceae; Bacillus; Bacillus REFERENCE 1	AUTHORS Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B. TITLE Delta-endotoxin genes and methods for their use JOURNAL Patent: WO 2004074462-A 15 02-SEP-2004; Athenix Corporation (US) FEATURES Location/Qualifiers 12073 /mol_type="unassigned DNA"	CDS / D. XTET="TaXON:1448" (DO XTET="1073 / Note="unnamed protein product" / Codon start=1	LSIIRKEVADSVLSDAIADFDGKLKNYREYYLSYLGAWLKDGKPLOKTNNSDIGGLVY YRKLSERDRENBILGGSLSRNNAQVLLLPFRQAANVOLLLLRDAVQYKAQWFPELSAE NVRSELISPNSGCDFTGDYSRLKCKTAEYTNYCLYWYQVGLNOIKGGGTGADTWSKF NKRRREMTLAVLDIIAIPPTYDPEKYPLTYNYCLYWYQVGLNOIKGGGTGADTWSKF NKRRREMTLAVLDIIAIPPTYDPEKYPLTYBLTREIYTDAVGYSGGTYSWLRNWPN TSNDLRNIDEQNADYYKTISELAINALVGFTTAREPRYSKAFBRRVGSPDLNYDAGNN GLSRWTIESTFPLYLHSNGVRGSBHRLSNAACVYGNSRVNYGWTHTSLKRENIIEA NQITQIPAVKSYYLQNYLANGVRGSBHRLSNAACVYGNSRVNYGWTHTSLKRENIIEA NQITQIPAVKSYYLQNYLANGVRGSBHRLSNAACVYGNSRVNYGWTHTSLKRENIIEA	ORIGIN Query Match 99.6%; Score 2073; DB 6; Length 2073; Best Local Similarity 100.0%; Pred. No. 0;	COMBELVACIVE TGAGTCCATATCAAAATAAAA TGAGTCCATATCAAAATAAAAA TGAGTCCATATCAAAATAAAAA TAACGCCAAACAGATATCCTT

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                                                               Tito,T., Sahara,K., Agano,S. and Bando,H.
Cloning and Expression of Novel Crystal Protein Genes from Bacillu, thuringieness subsp. aizawai Encoding a Mosquitocidal Proteins thuringieness subsp. aizawai Encoding a Mosquitocidal Proteins
L. Unpublished
E. 2 (bases 1 to 3746)
S. Ito,T., Sahara,K., Agano,S. and Bando,H.
Direct Submission
L. Submitted (14-Nov-2001) Takeshi Ito, Graduate school of Agriculture,Hokkaido University; Kita-9jyou Nisi-9chome, Kita-ku,Sapporo-shi, Hokkaido 060-8589, Japan
Kita-ku,Sapporo-shi, Hokkaido 060-8589, Japan
L. Location/Qualifiers
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     Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus, Bacillus
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Best Local Similarity 88.4%;
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                                CCTGATTTAAATTATGATGCAGGTAATAATGGGCTAAGCAGGATGACAATTGAATCTACG
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Ito,T., Sahara,K., Asano,S. and Bando,H.
Cloning and Expression of Novel Crystal Protein Genes from Bacillus
thuringiensis subsp. aizawai Encoding Mosquitocidal Proteins
Unpublished
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Direct Submission

Direct Submission

Direct Submitted (12-70N-2003) Takeshi Ito, Graduate School of

Agriculture, Hokkaido University, Department of Applied Bioscience;

Kita-9jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan

(E-mail:ito-t@abs.agr.hokudai.ac.jp, Tel:81-11-706-2487(ex.2487))
                                                                                                                                                                                                                                                                                                                                                                                                                                              AB112346 14-JUN-2003 Bacillus thuringiensis serovar aizawai cry40-like and ORF2 genes for putative mosquitocidal toxin, hypothetical protein, complete
                                                                                                                                                                                                                                            1445 ATGCGGCATGTTGTATATGGAAACTCCAGAGTTAACGTATATGGTTGGACACATACAA 1504
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                                                                                              1260 GAGAGATTAACGCTAGACCGGAGTATCGTGTTTCACGTGCAGAATTTAGTGAGTCAACAG
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                           TTGATTTTCAGAATGCCGATGTATATAAATTACTTCATTAGCTATCATGAACCTAGTAG
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/mol_type="genomic DNA"
/strain="Bun1-14"
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Bacillus thuringiensis serovar aizawai
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/transI_table=11
/product="putative mosquitocidal toxin"
/protein_id="BAC77648.1"
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Pred. No. 8.1e-125;
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LVTWLQAIDIYSHSINLQLGYLSGWGGTRHYEDPTXGNGAFQRWSGTTSNNPRNIIFG
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GPGPPRVERWSPSSVSNANFSRPATGGSYSFDYVDTLVTTFNQSGVEIIIQNLSGYHL
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GSGRTDCNERLKAKIKEYTNYCVGWYNKGLOQIRQATSAEVWSKFNKFRREWTLAVL
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Bacillus thuringiensis
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus
cereus group.
----GCTTGGGAAATACGAGGTACTAGCTCAGTTGTAGCAGGGCCTGGTCAT
                               CATACTGTTCAGCGTACGTTTTTCGGGTTCTATGACATATGATTCGTTTAAGTATTTAGAT
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                                                                                              AATAACAAAACTGCAGGACAAAGTTACCGTATTCGTTTTCGTTATGCTGCAGATAAAGCT
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Delta-endoctoxin genes and methods for their use
Patent: WO 2004074462-A 26 02-SEP-2004;
Athenix Corporation (US)
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/organism="Bacillus thuringiensis"
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/note="unnamed protein product"
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/db_xref="taxon:1428"
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WLQAIDIYSHSINLOLGYLSGNGGTHYRYBDFYRGNAFRQWAGGTTSNNBHNIIFGNTD
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Matches 1135; Conservative
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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Submitted (29-JAN-1997) Entomology, University of California, Boyce Hall, Riverside, CA 92521, USA Location/Qualifiers 1.0208 1.0208 /organism="Bacillus_thuringiensis serovar jegathessn"
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                                                                       /mol_type="genomic DNA"
/sub_species="jegathesan"
/db_xref="taxon:56955"
1. _2028
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Best Local Similarity 55.5%;
Matches 545; Conservative
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Bacillus thuringiensis jegathesan insecticidal protein Jeg74 gene,
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Kawalek, M.D. and Gill, S.S.
Isolation and characterization of insecticidal genes from Bacillus Unpublished
                                915
                                                                            Bacillus thuringiensis serovar jegathesan
Bacillus thuringiensis serovar jegathesan
Bacteria, Firmicutes; Bacillales; Bacillusceae; Bacillus; Bacillus
                                                                                                              TATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTTTTAATGGGTTAGAG
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Kawalek, M.D. and Gill, S.S.
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 CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCAAATATTATTTTTT
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Pred. No. 1.3e-20;
0; Mismatches 364; Indels 51;
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Bosch, H.J. and Stickema, W.J.
Genes encoding hybrid bacillus thuringiensis toxins
Patent: US 6780408-A 9 24-AUG-2004;
GEX;
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/organism="unknown"
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                                                                                                                            TATTATGATGATGATTAGCAAAATACGTTCACGAGGTTCAGATGGTGAACTTGGTGG
                                                                                                                                                                                                                               AAATTTAATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTT
                                                                                                                                                                                                                                                GAGTTTAATAAATTTCCTAGAGAGATGACATTAACGGTATTAGATCTTGTTGCATTATAT
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                                                                                                                                                                                                                                                                                                           AATTTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGAT
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TGGTATCAGGTATAAATCAGATAAAACAGGGGGGGGGCACAGGTGCTGACACTTGGTCG
                                             TTGAGTGCAGAGATGTAAGATCGGAATTAATATCACCTAACAGTGGTTGTGATTTTACC
                                                                                                         712 GGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 3468)

180sch, H.Jan. and Stiekema, W. Johannes.

Hybrid toxin
Patent: US 6204246-A 9 20-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
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Sequence 9 from patent US 6204246.
AR143378
AR143378.1 GI:15104664
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JOURNAL
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PF 01-JUL-1997 JP 1998504483
PI ERNEY H SCHNEPP, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI BRIAN A STOCKHOFF
PC C12N15/32, C12Q1/68, C12N15/82, C07K14/325, A01N63/00, A01H5/00 CC Strandedness: Single;
FT Topology: Linear;
FH Key Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                    AATTIGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                           AATAGGCGATGCAGGAAAGAAGGAGGATGTATTGGGACAACCATAGTCTCTTTATCAC 212
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Pred. No. 1.3e-20;
0; Mismatches 364;
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/organism="Homo sapiens"
                                                                                                                                                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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nes 458; Conservative
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                                      AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTATTATTGA 332
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                TCCGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGTGATTTATTATCTATAATTCG 329
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1 (bases 1 to 3471)
Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A. Toxins active against pests
Patent: JP 2001507208-A 42 05-JUN-2001; PN JP 2001507208-A/42
PN JP 2001507208-A/42
                                                                                             TAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTTTTGACGGTAAATTGAA
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Schnepf, H. Ernest., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and Muller-Cohn, J.
Toxins active against pests
Patent: US 6369213-A 71 09-APR-2002;
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CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCAAATATTATTT
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Best Local Similarity 52.5%; Pred. No. 1.3e-20;
Matches 458; Conservative 0; Mismatches 364; Indels
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1. .3471
/organism='Unidentified'
Location/Qualifiers
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Patent: JP 2002500166-A 42 08-JAN-2002;
WYCOGEN CORP
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DN JP 2002500166-A/42
PD 08-JAN-2002
PD 08-JAN-2002
PR 31-DEC-1999 UP 200526647
PR 31-DEC-1999 US 09/002285
PT ERNEST H SCHNEPF, CAROL WICKER, KENNETH
                     990 INGGITACGGAATIGGCCTAATACTTTTAATGG 1022
                                                              948 raddegaaaagriddriragcrirgriaarad 980
                                                                                                                                                                          Toxin active on Ostrinianubilalis.

    .3471
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Schnepf, E.H., Wicker, C.,
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                               AATAGGGGATGCAGCAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTTATCAC 212
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Unclassified.

1 (Dases 1 to 3471)

2 Schnegf,H.E., Wicker,C., Narva,K.E., Walz,M. and Stockhoff,B.A.
Toxins active against pests
Patent: US 6570005-A 71 27-MAY-2003;
Mycogen Corporation; Indianapolis, IN
                                           AAATTATAGAGAGTATTATCTTTCTTTGGGGCTTTGGCTTAAAGACGGTAAACCACT
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Best Local Similarity 52.5%; Pred. No. 1.3e-20;
Matches 458; Conservative 0; Mismatches 364;
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AL10345 Drosophil
BH137139 ENTNZ29TF
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CW954723 TCB44.2
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mall : segref@genoscope.cns.fr
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BL502178 kt86c11.y
ALG6837 Crosophil
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Birect Submission

Direct (Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattoriegec.riken.jp, VRL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-911, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp
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/clone_lib="MSMg01 Mouse Male BAC Library"
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2.7%; Score 56; DB 10; Length 20
Best Local Similarity 45.6%; Pred. No. 0.038;
Matches 194; Conservative 0; Mismatches 231; Indels
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   14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-124J02.T7"
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1. .2087
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Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain CS7BL/60, as defined by BAC-end sequence-SNP analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                  ATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAATACACTA
                                                                                                                                                                        367 GCAGAITITGACGGTAAATITGAAAATTATAGAGAGTATTATCTTTGTGGGGCT
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   Length 1101;
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Query Match
3.2%; Score 67; DB 10; L
Best Local Similarity 16.8%; Pred. No. 8.3e-05;
Matches 113; Conservative 278; Mismatches 282;
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Lubrited (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- web. suww.genoscope.cns.fr)
- web. suww.genoscope.cns.fr)
- betermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Biffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoral digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACRSP01 of RPCI-98 library from Drosophila melanogaster (fruit AL069440
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Similarity 36.2%; Pred. No. 0.17;
34; Conservative 62; Mismatches 279; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Backeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP pl and bw to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                         CNSVUOUI 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACK01016 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
                                                                                                    fly), genomic survey sequence.
AL065414
AL065414.1 GI:4938827
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/clone lib="RPCI-98"
/note="end : TET3"
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the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                     2.5%; Score 52.8; DB 9; Length 8 45.9%; Pred. No. 0.18; tive 0; Mismatches 212; Indels
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/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica State in Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for
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Entamoebidae; Entamoebidae; Entamoeba.

E (bases 1 to 874)

Loftus, B., Van Aken, S. and Fraser, C.

Entamoetidae; Entamoeba.

E I (bases 1 to 874)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1: MSS sheared DNA library

Loftact: Brendan J Loftus

Confact: Brendan J Loftus

Confact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 9208

Fax: 301 838 3543

Email: bjoftus@tigr.org

Clones are derived from the Entamoeba histolytica HM1: IMSS sheared

DNA library

Seg primer: M13-Forward
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                                                                                                                                                                                                                                                                   263 AACTAATTCCGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGTGATTTATTATCTA 322
                                                                                                                                                                                                                                                                                                                                                                                                TAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTA 382
          TCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTA
                                                                                                                                                                                                       TTWAWATTTTAAATAWATTTAATTTAAWTTAWWTWTTTAAWAWTTTAAWTATTAAARWWAA
                                                                                                                                                                                                                                                                                                            881 ATWAAATTAWWTTAAAAWAATGWTTTWTAAATTWWGTTAWTTTTTTATTTTWAAATTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821 WATATWATRTAAATTWTATWYTTTTWTTTAAWATTTTTAWATTTAWWTAAWAWTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTGAAAAATTATAGAGAGTATTATCTTTCTTATCTTGGGGCTTGGCTTTAAAGACGGTA
                                                                                                                                       TAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAATACACTATTATCAATAATAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 CAGAAAGAGATTTCAATGAAATTCTAGGAGGGTCATTGTCAAGAAACAATGCTCAA 558
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AZ533618
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High quality sequence start: 41
High quality sequence stop: 761.
Location/Qualifiers
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/strain="HM1:IMSS"
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Los Drosophila melanogaster genome survey sequence TET3 and of BAC #BACR28K21 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1186 ACGAGTAATGATCTACGTAATATTGATTTTCAGAATGCCGATGTATAAAAATTACTTCA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            950 TITATACAGATGCAGTGGGATATICATCGGGAACTTATAGTTGGTTACGGAATTG---G 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 TGTGCAGTTATTACTATTAAGGGATGCAGTTCAATATAAAGCACAATGGTTCCCATTTTT
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                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                   267;
                                                                                                                                                                                                                                                                                                                                         h 2.5%; Score 51.6; DB Similarity 17.2%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                114; Conservative 273; Mismatches
                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03G04"
/clone lib="brosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                         organism="Drosophila"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDCP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etudé du Polymcrhoisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence SP6 end of BAC BACNOSGO4 of DrosBAC library from Drosophila melanogaster (fruit AL098379
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or hybridization from the BACPAC Resource Center can http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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                                                                                                              /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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/clone="BACR29B23"
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                                                                                                                                                                                                                                                                                                                                                        Query Match
2.5%; Score 52.2; DB 10;
Best Local Similarity 33.7%; Pred. No. 0.27;
Matches 136; Conservative 73; Mismatches 191;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.

E | Chasses | Lo 548)

McCarter, O., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
McCann, R., Waterston, R. and Wilson, R.,
The Washington Univ. Nematode EST Project, 1999

L Unpublished (1999)

Contact: McCarter JP

The Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1800
           kt86c11.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter Strongyloides ratti cDNA 5' similar to TR:Q18989 Q18989 D2045.9 BI502178
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He library was constructed by Brandi Chiapelli and Dr. James

McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)

Washington University, St. Louis. DNA Sequencing by: Washington

University Genome Sequencing Center St. Louis.

High quality sequence stop: 395.

Location/Qualifiers
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McCarter"
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44.9%; Pred. No. 0.56;
***** 0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Strongyloides ratti"
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                                                                                                                                                                                   BIS02178.1 GI:15352567
                                                                                                                                                                                                                                        Strongyloides ratti
Strongyloides ratti
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RESULT 9
BIS02178
LOCUS
DEFINITION
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                                                                                                                                                                      Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EWRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecox digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 TAATTAAAATATATTATAAAAWWAAATGGATTTTGGGTTAAATAATAATAWGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 TIGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGA
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                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity 41.6%; Pred. No. 0.46;
Matches 187; Conservative 29; Mismatches 228;
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/db_xref="taxon:7227"
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/clone lib="RPCI-98
/note="end : TET3"
                                                                                                                                                           Genoscope
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M. Catter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Wylie, T., Dante, M., Ritter, E., Bennett, J., Franklin, C., Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., McCann, R., Waterston, R. and Wilson, R., The Washington Univ. Nematode EST Project, 1999

L. Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 bp mRNA linear EST 09-MAY-2001
TBN95TM-SSR Strongyloides stercoralis cDNA 5', mRNA
                                         862
                                                                                                                                     802
                                                                                                                                                                                    652
                                                                                                                                                                                                            713 GTGATTACTATGAG-CGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATAT 771
                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (funtmamenih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 411.
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/lab_host="taxon:6248"
/lab_host="xL-1 Blue MRF" (Stratagene)"
/clone lib="TBN957M-SSR"
/note="vector: Lambda Uni-ZAP XR (Stratagene); Site 1:
ECORI; Site 2: Xho1; mRNA was purified from 2 x 1083
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the ECORI site to the XhoI site. The library
AATTAGTTTATTATTATAACTTTCAGAAAGAGATTTCAATGAAATTCTAGGAGGGTCAT
                     TGTCAAGAAACAATGCTCAAGTATTGTTATTACCTACT-----TTTGCACAAGCTGCAA
                                                                                                             ATGTGCAGTTATTACTATTAAGGGATGCAGTTCAATATAAAGCACAATGGTTCCCATTTT
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/mol_type="mRNA"
/strain="Rhabditiform larvae obtained from gerbils"
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Panagrolaimoidea, Strongyloididae, Strongyloides.
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Direct Submission
Submitted (23-UU1-1999) Genoscope - Centre National de Sequencage :
Submitted (23-UU1-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Generieve Payan. It has been constructed in the vector
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            TTTAAACTTTCAGAAAGAGATTTCAATGAAATTCTAGGAGGGTCATTGTCAAGAAACAAT 552
                                                                                                                                                                                                                                            TITCTATATGTGATITTATTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTG 358
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                                                                                                                                             414 TACCCAATTCCAAATAGATTTTCTTTTGATAAATTTTAATTTAATTTAAAAGAAGA
                                                       354 AATAGAATTTCAGAAGGTGATTTGTATTTTACCATCATCTAAAATTTTTAAAAATCT
                                                                                                   GCTCAAGTATTGTTATTACCTACTTTTGCACAAGCTGCAAATGTGCAGTTATTACTATTA
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/organism="Drosophila melanogaster"
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llarity 23.7%; Pred. No. 0.64;
Conservative 181; Mismatches 210;
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/db_xref="taxon:7227"
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/clone lib="brosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovy Osoogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; chw by, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bccpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSO06N9 964 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J19 of RPCI-98 library from Drosophila melanogaster (fruit
vector from the Ecors aite to the XhoI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E1 pfu/ml. The average insert size of the unamplified to feet of 9 x 10E11 pfu/ml. The faverage insert size of the unamplified library is 675 bp (range, 100-1700)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AGATTGATTCAATAGAAATGAATTAGAAGGTGGTGGTATTATAAAAATTTTAGAAATA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 ragacaagrcaagraaragraarrcagarrcagarggraacaacaaaaraaraaaarg 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 AGACATTCAAAGGATACTCCTCAGGAAATTCACACCTTGACATTGATGATTTAAAAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 ATTCTGATATCGGACAATTAGTTTATTATTTTAAACTTTCAGAAAGAGATTTCAATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                             344 ATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAAATTGAAAATTATAGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 ATTATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TICTAGGAGGGTCATTGTCAAGAACAATGCTCAAGTATTGTTATTACCTACTTTTGCA
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Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                Length 520;
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Best Local Similarity 50.6%; Pred. No. 0.7;
Matches 121; Conservative 0; Mismatches 118; Indels
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR14J19"
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/note="end : T7"
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L. Unpublished (1999)

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The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
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The library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (tnutman@mih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             105 AGATTGATTCAATAGAAATGAATTAGAAGGTGGTGTATTATAAAAATTTTAGAAATA 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 ATTCTGATATCGGACAATTAGTTTATTTTTAAACTTTCAGAAAGAGATTTCAATGAAA 523
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ECORI; Site_2: XhoI; mRNA was purified from 2 x 1083
rhabditform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. CDNA was constructed
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                                                                                                                                                                                                                                                                                                                                                  344 ATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAAATTGAAAATTATAGAGAGT
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/mol_type="mRNA"
/gtrain="Rhabditiform larvae obtained from gerbils"
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Panagrolaimoidea; Strongyloididae; Strongyloides.
1 (bases 1 to 520)
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/lab_host="XL-1 Blue MRF' (Stratagene)"
/clone_lib="TBN95TM-SSR"
                                                                                                                                                                                                                     2.4%; Score 50.2; DB 2; 50.6%; Pred. No. 0.69; iive 0; Mismatches 118;
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Strongyloides stercoralis
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Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
176 Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
1713 330 838 9268
1721 Eax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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ENTQG77TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 923)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
Unpublished (2001)
                                                          4 AAAAAGATGAGTCCATATCAAAATAAAAATGAATATGAAATATTGGAATCCTCATCGAAT
                                                                                       AACACAAATACGCCAAACAGATATCCTTTTGCAAATAATCGGGATATGTCTACTATGTCT
                                                                                                                                       TGGAATGATTGTCAGGGAATCTCATGGGATGAAAT--TTGGGAATCAGTCGAAACGATAA
                                                                                                                                                                                                     CAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAATA
                                                                                                                                                                                                                                                                                                        242 CACTATTATCAATAATAGGAAAACTAATTCCGACTAATCGTCAAACTGTGTCAGCACTTT
                                                                                                                                                                                                                                                                                                                                                                     302 CTATATGTGATTTATTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAGTGATG
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ن
   DB 10; Length 964;
Query Match 2.4%; Score 50; DB 10; Length 96
Best Local Similarity 30.9%; Pred. No. 0.87;
Matches 137; Conservative 108; Mismatches 195; Indels
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The Institute for Genomic Research
Tylz Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0208
Fax: 301 838 3543
Eaxil: bjoftusetigr.org
Clones are derived from the Entamoeba histolyt
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Mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Class: shotgun
High quality sequence stop: 658.
Location/Qualifiers
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bar 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, LiS. (1993) Entamoeba histolytica: a
method for isolate dentification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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1 (bases 1 to 892)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HMI:IMSS sheared DNA library
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Entamoeba histolytica
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us-10-781-979-2.rst

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l. .892
/mol_type="genomic DNA"
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/db_xref="taxon:5759"
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/doctor: ph051; Site 1: Bst 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically phase for tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotqun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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DNA library
Seg primer: M13-Reverse
Class: shotgun
High quality sequence start: 29
High quality sequence stop: 688.
Location/Qualifiers
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Aev1522 Bacillus
Aev89221 Bacillus
Aes02489 Ecillus
Aex39905 Truncated
Aev39758 Echurin
Aev93756 Bacillus
Abv93756 Bacillus
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Abv93757 B. thurin
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Aev83877 Bacillus
Aex83877 Bacillus
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Aex99886 Nucleocid
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Aev86782 Insectici
Aev89886 Nucleocid
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Aav83927 DNA encod
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AAH26983
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1. .2082
/*tag= a
/product= "AXMI-008"
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2003US-0448812P.
19-FEB-2004; 2004US-007812P.
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782191.
19-FEB-2004; 2004US-00782191.
19-FEB-2004; 2004US-00782191.
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 WO2004074462-A2
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 ADR89401;
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Adr89413 AXMI-008
Adr89414 AXMI-008
Adr89416 AXMI-008
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Adr89418 B. thurin
Abx13497 B. popill
Abb0830 Paenibaci
Adr89411 AXMI-009
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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                                                                           New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
                                                                                                                                           This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start condons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidoteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin acting the presence of delta-endotoxin or delta-endotoxin.
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tive 0; Mismatches
                       Duck
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Matches 2082; Conservative
                      Hargiss T,
ATHENIX CORP
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P-PSDB; ADR89402.
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GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAATTCTGATATCGGACAA

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TTAGTTTATTATTAAAACTTTCAGAAAGAGATTTCAATGAAATTCTAGGAGGGTCATTG

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ttagtttattattattaaacttticagaaagagatttcaatgaaattctaggagggtcattg tcaagaaacaatgctcaagtattgttattacctacttttgcacaagctgcaaatgtgcag

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New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGAAAAAGATGGAGTCCATATCAAAATAAAAATGAATATGAAATATTGGAATCCTCATCG 227
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                                                                                                                                                                                              This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin or delta-endotoxin.

The second of delta-endotoxin or delta-endotoxin-associated proteins or presence of delta-endotoxin or delta-endotoxin-associated proteins or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240
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100.0%; Pred. No. 0;
cive 0; Mismatches 0; 3
     NB,
     Duck
                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids in products or organisms.
                                                                                                                                                                Claim 1; SEQ ID NO 12; 178pp; English.
     Koziel MG,
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Best Local Similarity 100.
Matches 2082; Conservative
   Hargiss T,
                                      WPI; 2004-635574/61.
P-PSDB; ADR89402.
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                   GCAGGTGGCGGAATTAGATTATTAATAACAAAACTGCAGGACAAAAGTTACCGTATT
                                                                                                                                                                                                                   GCAGGTGCCGGAATTAGATTGATTAATAACAAAACTGCAGGACAAAGTTACCGTATT
                                                                                                                                           TGGGGTTCAAATCGTTTTGTATCGCTTGAAAAATCTTACTCTGGAAATTATGACGATTTA
                                                                                                                                                                                                                                                AAATATAGTGATTTTAAATTCGCTGAAATTATCACACCCCCCATTACCTAGTTCAAACATT
                                                                                                                                                                                                                                                                                                                                                                   AAAATTGAATTCCTCCCCAAGTAATACAACTTTAGAATATGAGGGAGAACGGGACCTA
                                                                      CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTGTATATCTTTATCCAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_except= pos:168. .170, aa:Met
                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAAAACAAAGAACGCGGTGAACGATCTGTTTACCAATTAA
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168. .2249
/*tag= a
/product= "AXMI-008"
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
30-FEB-2004; 2004US-007812P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-0078219.
19-FEB-2004; 2004US-0078219.
19-FEB-2004; 2004US-0078219.
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CAGATGGATGTGGAGATGCGAATAGTTTTCAATCAGATGTAAACGTGGTTCTCGAC 1980
GCAGGTGGCGGAATTAGATTGATTAATAACAAAACTGCAGGACAAAGTTACCGTATT 1907
                                 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTATCCAGGAGGT
                                                                          AAATATAGTGATTTTAAATTCGCTGAAATTATCACACCTCCATTACCTAGTTCAAACATT
                                                                                                                       AAATATAGTGATTTTAAAATTGGCTGAAATTATCACACCTCCATTACCTAGTTCAAACATT
                                                                                                                                                                2088 CAGATGGATGTGGAGATGCAAGCGAATAGTTTTCAATCAGATGTAAACGTGGTTCTCGAC
                                                                                                                                                                                               1981 AAAATTGAATTCCCCCCAAGTAATACAACAACTTTAGAATATGAGGGGGAAGGTA
                                                                                                                                                                                                           2148 AAATTGAATTCCCCCCAAGTAATACAACAACTTTAGAATATGAGGGAAGAACGGGACCTA
                                                                TGGGGTTCAAATCGTTTTGTATCGCTTGAAAAATCTTACTCTGGAAATTATGACGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                        ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance; pesticidal activity.
                                                                                                                                                                                                                                           GAAAAAACAAAGAACGCGGTGAACGATCTGTTTACCAATTAA 2082
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/*tag= a
/product= "Alternative AXMI-008"
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448630P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782141.
19-FEB-2004; 2004US-00782141.
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P-PSDB; ADR89404

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

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Claim 1; SEQ ID NO 15; 178pp; English

This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delt nucleic acids in products or organisms.

Sequence 2073 BP; 694 A; 305 C; 431 G; 643 T; 0 U; 0 Other;

ô Gaps ö Length 2073; Indela DB 13; ö 99.6%; Score 2073; D 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 2073; Conservative Query Match ઠે

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1080 1149 1200 1260 1389 1689 1029 1750 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTTATCCAGGAGGTTGGGGTTCA 1809 720 789 849 909 900 969 960 AGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAG TATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTTTTAATGGGTTAGG GATTTTCAGAATGCCGATGTATAAAATTACTTCATTAGCTATCAGAACCTAGGA GAGTATGTTTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAAGACTACACA AAGGGTAACGGTATTTTCAACGTATGTCTGGAACTACGAGTAATGATCTACGTAATATT GAGACTACCGCTAGACCAGAGTATCGTGTTTCAAAGGCAGATTTTCGTAGGGTAGGGGGA CCTGATTTAAATTATGATGATGAGGTAATAATGGGCTAAGGAGGATGACAATTGAATCTACG TTCCCACTTGTATTGCACTCTAATGGTGTTAGAGGACCCTCTCATAGATTATCAAATGCG 1441 GCATGTGTATATGGAACTCCAGAGTTAACGTATATGGTTGGACACATACAAGTTTA AATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAATAAATTTCGT GAGTATGTTTCGAGATATTTTGCCGGCTGGGTAGGAACTCGTCATTATGAAGACTACACA AAGGGTAACGGTATTTTTCAACGTATGTCTGGAACTACGAGTAATGATCTACGTAATATT GATTTTCAGAATGCCGATGTATAAAATTACTTCATTAGCTATCATGAACCTAGTAGGA GAGACTACCGCTAGACCAGAGTATCGTGTTTCAAAGGCAGATTTTCGTAGGGTAGGGGGA TTCCCACTTGTATTGCACTCTAATGGTGTTAGAGGACCCTCTCATAGATTATCAAATGCG GCATGTGTTGTATATGGAAACTCCAGAGTTAACGTATATGGTTGGACACATACAAGTTTA AAACGTGAAAATATAATTGAAGCCAATCAAATTACACAAAATACCGGCGGTGAAGGTTAT CCTGATTTAAATTATGATGCAGGTAATAATGGGCTAAGCAGGATGACAATTGAATCTACG **AAACGTGAAAATATAATTGAAGCCAATCAAATTACACAAATACCGGCGGTGAAGAGTTAT** TACCTTCAAAATTATCTTGCTAATGCCTATACCTATGTAATAAAAGGCACTCATACAGGT 1681 GGAATTAGATTGATTAATAACAAAACTGCAGGACAAAGTTACCGTATTCGTTTTCGT 1030 1021 1090 1081 1150 1201 1261 1330 1450 1510 1501 1570 1561 661 730 721 790 781 850 841 910 901 970 961 1270 1321 1390 1381 1690 1141 1210

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This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pestes. Compositions containing the delta-endocoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or
New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
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Pred. No. 9.9e-160;
0; Mismatches 423; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;
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                                                                                Claim 1; SEQ ID NO 26; 178pp; English
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Best Local Similarity 69.8%;
Matches 1143; Conservative
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  ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance;
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/*tag= a
/product= "AXMI-008"
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1. .2019
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; 2003US-0448633P.
; 2003US-0448107P.
; 2003US-044810P.
; 2003US-0448112P.
; 2004US-00781979.
; 2004US-00782020.
; 2004US-00782020.
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P-PSDB; ADR89415.
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240 300 300 360

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/*tag= a /product= "AXMI-008" /transl_except= pos:127.

2004WO-US005829

Location/Qualifiers

(first entry)

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ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance; pesticidal activity.
                      AXMI-008 full length coding sequence
                                                                                                                                                                                                                                                        20-FEB-2003; 2003US-0448632P.
20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448863P.
20-FEB-2003; 2003US-0448810P.
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19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782141.
19-FEB-2004; 2004US-00782141.
                                                                                                   Bacillus thuringiensis.
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P-PSDB; ADR89415.
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                     TATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGTATCAG
                                                                                                                                                                    CCAGTGGGATATTCAGGGGGAAATTATGGTTGGGAACGGTTTT-----TTAGCTTTAAT
  ---CTGATTGT
                                         676 AACGAGGGTTAAAAGCGAAAATAAAAGAGTATACTAATTATTGTGTAGGGTGGTATAAC
                                                                GTAGGTTTAAATCAGATAAAACAGGGGGGCACAGGTGCTGACACTTGGTCGAAATTTAAT
                                                                                                            AAATTICGTAGAAATGACGTIGGCGGTATTGGATATTATCGCTATATTICCAACTTAT
                                                                                                                                                       GATITIGAGAAATATCCATIGCCAACACATGTAGAGTIGACTAGGGAAATTIATACAGAT
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This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for sepecifically bacteria and plants. These organisms are useful for associated or improved delta-endotoxin or delta-endotoxin or delta-endotoxin.
isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids in products or organisms.
                                                                                                                                                            Claim 1; SEQ ID NO 25; 178pp; English.
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ADR89413 standard; cDNA; 2145

ADR89413 RESULT

ADR89413

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1513 AATTACTCTCATAGATTATCAAATGCGGCATGTGTTCAAAATGAAACCTCCAGAGTTAAC 1572
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                      CATTATGAAGACTTCACAAAGGGTAACGGTGCTTTTCAACGTACGAACTACGAACTACGAGT
                                                                                                                                                        A---TCATGAACCTAGTAGGAGAGACTACCGCTAGACCAGAGTATCGTGTTTCAAAGGCA
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CATTATGAAGACTACACAAAGGGTAACGGTATTTTTCAACGTATGTCTGGAACTACGAGT
                                                                                                   1396 GAATITITICCGACACACTAAATACTITICCTGTATGAGGTAAACAGTTCTGGG---TAC
                                                                             AATGATCTACGTAATATTGATTTTCAGAATGCCCATGTATATAAAATTACTTCATTAGCT
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1. .2010
/*teg= a /product= "Alternative AXMI-008"
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-044806P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2004US-007812P.
19-FEB-2004; 2004US-00781979.
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                                                                                                                                                                                                                                                                                                                                                                              endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for Killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin or delta-endotoxin.
                                                                                                                                                                                                                                        isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATTCTGATATCGGACAATTAGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes an isolated delta-endotoxin. Some of the delta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 2010 BP; 657 A; 324 C; 417 G; 612 T; 0 U; 0 Other;
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Pred. No. 4.8e-158;
0; Mismatches 422;
                                                                                                                                           Duck NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids in products or organisms.
                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 28; 178pp; English.
                                                                                                                                         Koziel MG,
; 2004US-00782096.
; 2004US-00782141.
; 2004US-00782570.
; 2004US-00783417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.77
Matches 1135; Conservative
                                                                                                                                         Hargiss T,
                                                                                                   (ATHE-) ATHENIX CORP
                                                                                                                                                                            WPI; 2004-635574/61.
P-PSDB; ADR89417.
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                    19-FEB-2004;
19-FEB-2004;
19-FEB-2004;
                                                                                                                                         Carozzi N,
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AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT 269
                                                                                                                                             TAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAAATTGAA 389
                                                                                                                                                                              319 TTTACGGGTAAGTCAGAGTGTTTTAAATGATGGGATTGCAGATTTTAATGGTTCTGTACT 378
                                                                                                                                                                                                                                                   379 CTTATACAGGAACTATTTAGAGGCTCTGGATAGCTGGAATAAGAATCCTAATTCTGCTTC 438
                                                                                                                                                                                                                                                                                                                       439 igcrgaagaacrccgiacrcgiriragaarcgccgacrcagaarirgaragaarrrraac 498
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTACTITIGGACAAGCTGCAAATGTGCAGTTATTACTATTAAGGGATGCAGTTCAATA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAAGCACAATGGTTCCCATTTTTGAGTGCAGAGAATGTAAGATCGGAATTAATATCACC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 TAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GAACT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTAGAGTTGACTAGGGAAATTTATACAGATGCAGTGGGATATTCATCGGGAACTTATAG 989
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                                   <u>agcaccirciraciggariaarircaaragrargacciraraggraaagracragg</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plants; pest control; crop protection;
                                                                      270 TCCGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGTGATTTATTATCTATAATTCG
                                                                                                                                                                                                                                                                                                                                                                                 CCGAGGGTCTTTAACGAATGGTGGTCGTTAGCTAGACAAAAATGCCCAAATATTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            754 CACTAGIGCTACAGCTIGGTTAGAATTICATAGATATCGTAGAGAGAIGACATGATGGT
                                                                                                           AGGTAGTAGTAGACAATCCATATCAGATTTGTCTATATGTGACTTATTATTGA
                                                                                                                                                                                                                 390 AAATTATAGAGAGTATTATCTTTGTTGGGGCTTGGCTTAAAGACGGTAAACCACT
                                                                                                                                                                                                                                                                                        TCAAAAGACAAATAATTCTGATATCGGACAATTAGTTTATTATTAAACTTTCAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGGATATTATCGCTATATTTCCAACTTATGATTTTTGAGAAATATCCATTGCCAACACA
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                                                                                                                                                                                                                                                                                                                                                           AGATTICAATGAAATICTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAGGIGCIGACACTIGGICGAAATITAATAAATITICGIAGAGAAATGACGITGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGGITACGGAATIGGCCTAAIACTITIAAIGG 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGGGGAGAAGTTGGTTTAGCTTTGTTAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoding native Cry9Aa toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGCTTATT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ93235 standard; DNA; 3837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cry9Aa; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003
04-JUL-2000
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IID AAZ2
XX AAZ3
XX AAZ3
XX DT 15-6
DT 04-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic DNA sequences derived from the sequence of the truncated cry9ha gene of Bacillus thuringiensis ssp. galleria can be used for the production of a unique insecticidal protein having the same properties as the N-terminal domain of the insecticidal protein encoded by the native cry9ha gene of Bacillus thuringiensis ssp. galleria. The insecticidal toxin works by binding to specific receptor molecules in the gut of insects with consequent formation of ion channels in the epithelium. This action leads to ion efflux and paralysis of the intestinal function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which causes death of the insect. The synthetic DNA sequences exhibit enhanced expression through improved mRNA processing, stability, and/or translation providing improved tolerance against target insects. They can be used in the production of transgenic plants capable of expressing the N-terminal domain of the insecticidal protein encoded by the native cry9Aa gene. They therefore have a role in pest control and crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AATTIGGGAATCAGICGAAACGATAACAAGIATIGGGATAAATCTIATAGAGITTGTGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified synthetic DNA sequences comprise modification of the truncated cry9Aa gene of Bacillus thuringiensis for improved insect control in plants.
                                                                                                                                                                                                                                                              Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 170.2; DB 3;
llarity 52.6%; Pred. No. 1.3e-28;
Conservative 0; Mismatches 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pehu
                                                                                                                                                                                                                                Sequence encoding truncated Cry9Aa toxin.
                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis; ssp. galleria
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
17. .1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 55-57; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koivu K,
                                                                                                                          BP
                                                                                                                        AAZ93234 standard; DNA; 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-FI000698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98FI-00001809
                                                                                                                                                                                           (first entry)
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                                   1575
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P-PSDB; AAY83039.
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                               1567 GCTGGGCCT
1612 AAAGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 459; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200011025-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1998;
                                                                                                                                                                                           04-JUL-2000
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                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                          AAZ93234;
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                                                                                                         AAZ93234
                                                                                       RESULT
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Bacillus thuringiensis; ssp. galleria.

139 AATAGGCGATGCAGCAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTTATCAC 198

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957 ACCTICTITIGGAGGGCTGCATTITICCATTIATTACTACTAAGGGATGCTACTAGATA 1016
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                                                                                                                                                                                                                       1017 itsecactrairitesesetrirecarsetraciaesetririaraartraicaareaaetrasi 1076
                                                                                                                                                                                                                                                                                                                 1077 AGAGCTTATT-----GAACT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1272 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAATTGGTTTTGTACATCGTAGTAGTCT 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGGATATTATCGCTATATTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA 929
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                                                                                                                                                                                                                                                                                                                                                              750 GTATACCAATTATTGTTTATTGGTATCAGGTTTTAAATCAGATAAAACAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    897 CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCAAATATTATTATT
                                                                                         TAAAGCACAATGGTTCCCATTTTTGAGTGCAGAGAATGTAAGATCGGAATTAATATCACC
                                                                                                                                                                                                                                                                    690 TAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                        1092 ATATACTGATTATTGCGTACATTGGTATAATCGAGGTTTCAACGAACTAAGACAAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1212 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTACCCAATAGAAACAGA
510 AGATTTCAATGAAATTCTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin, lepidopteran pest; control; Agrotis ipsilon; black cutworm;
Heliothis virescens; Helicoverpa zea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a Bacillus thuringiensis toxin designated 86BB1(a).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .3471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic DNA sequences derived from the sequence of the truncated cry9Aa gene of Bacillus thuringiensis ssp. galleria can be used for the production of a unique insecticidal protein having the same properties as the N-terminal domain of the insecticidal protein encoded by the native cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal toxin works by binding to specific receptor molecules in the gut of consects with consequent formation of ion channels in the epithelium. This action leads to ion efflux and paralysis of the innestinal function, which causes death of the insect. The synthetic DNA sequences exhibit can branced expression through improved mRNA processing, stability, and/or translation providing improved tolerance against target insects. They can be used in the production of transgenic plants capable of expressing the used in the production of transgenic plants capable of expressing the cry9Aa gene. They therefore have a role in pest control and crop protection. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠, *
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                                                                                                                                                                                                                                                                                                                                                           Pehu E;
                                                               /*tag= a
/product= "Cry9Aa toxin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 57-59; 90pp; English.
                Location/Qualifiers
385. .2364
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                                                                           (PSBĞBB1). It encodes a toxin designated 86BB1(a) which is active against lepidopteran pests. The toxin isolates can be used for the control of lepidopteran pests such as Agrotis ipsilon (black cutworm), Heliothis virescens and Helicoverpa zea. PCR primers and probes can be derived from the polynucleotide encoding the toxin and used for the amplification and detection of other toxin-encoding sequences
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                                                            sequence is isolated from a Bacillus thuringiensis isolate
                                                                                                                                                                                                                                                                                    AATTTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGAT
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                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                       Length 3471;
                                                                                                                                                                                      Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                    Score 168.6; DB 2;
Pred. No. 3.5e-28;
0; Mismatches 364;
                               5; Page 86-88; 183pp; English
                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.5%;
Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          693 AGAGCTTATT----
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AATAGGCGATGCAGCAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTTATCAC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method has been developed for the control of European corn borer (Ostrinia nubilalis), comprising contacting the pest with a pesticidal amount of a Bacillus thuringiensis toxin. The method is used for the control of European corn borer (Ostrinia nubilalis). The method can also be used for the control of other non-mammalian pests, particularly black cutworm, and other lepidopteran pests. The present sequence encodes a Bacillus thuringiensis toxin from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for control of European corn borer using Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                 thuringiensis; toxin; Ostrinia nubilalis; lepidopteran; corn borer; black cutworm; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 168.6; DB 2; Length Pred. No. 3.5e-28; Mismatches 364; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BA;
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TTGGTTACGGAATTGGCCTAATACTTTAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Scor.
52.5%; Pred
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                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                          thuringiensis toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US026585.
                                                                                                                                                                                        3471
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Matches 458; Conservative
                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis
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P-PSDB; AAY24959.
                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9933991-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-DEC-1997;
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Rupar MJ;

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The sequence encodes a B. thuringiensis Lepidopteran-active delta-endotoxin, crystal protein CryBT60. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polymuclectides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, octton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, to legume, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
                                                                                                                                                                                                                                                       Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 127-128; 173pp; English
                                                                                                                                                    Baum JA, Chu C, Donovan WP,
                           13-SEP-2000; 2000WO-US025361
                                                                    99US-0153995P
                                                                                                                                                                                                                                                                                                  insect resistance of plant.
                                                                                                                                                                                           WPI; 2001-281518/29.
                                                                                                             (MONS ) MONSANTO CO
                                                                                                                                                                                                                P-PSDB; AAU02035
                                                                    15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delta endotoxin; Lepidopteran-active; crystal protein; insecticide; transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET60; ds.
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                                                                TCAAAAGACAAATAATTCTGATATCGGACAATTAGTTTATTATTTAAACTTTTCAGAAAG
                                                                                                         TGCTGAAGAACTCCGTACTCGTTTTAGAATCGCCGACTCAGAATTTGATAGAATTTTAAC
                                                                                                                                                                                      CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCAAATATTATTA
                                                                                                                                                                                                                               ACCTACTTTTGCACAAGCTGCAAATGTGCAGTTATTACTATTAAGGGATGCAGTTCAATA
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note= "No stop codon"
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/product= "CryET60"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 AGGTAGTAGTAGAACCATATCCATATCAGATTTGTCTATATATGAGTAGTATTATTATTATTGA
                                                                                                                                                                                                                                                                                                                                                                213 AGCACCTTCTCTTACTGGATTAATTTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG
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                                                                                                                                                156 AATTTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGAT
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                                                                                 Gape
                                                                             51;
Query Match
Pest Local Similarity 51.9%; Pred. No. 2.1e-26;
Matches 453; Conservative 0; Mismatches 369; Indels 51;
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22-MAR-2001

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CAGATGCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTT 1015
which has larval growth inhibiting or insecticidal effect in members of the Scarabaeidae insect family. The polypeptides and agents derived from the polypeptides of the invention are useful for controlling Scarabaeidae insects. Larvae of the Scarabaeidae insects eat the roots of a wide variety of plants e.g turf, agricultural or horticultural crops and trees, causing serious damage. This sequence encodes a polypeptide associated with the parasporal body contained in the sporangia of porteinaceous aggregate which comprises one kind or different kinds of polypeptides. The products of the invention have been shown to have a standardise OS field)
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58.0%; Pred. No. 4.1e-13;
iive 0; Mismatches 141;
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04-JUL-2001; 2001JP-00203463.
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Scarabaeidae; turf; agricultural crop; tree; proteinaceous aggregate;
Anomala cuprea; horticultural crop; gene; ds.
                                                                                                                                                                                                              GTATACCAATTATTGTTTATATTGGTATCAGGTAGGTTTAAATCAGATAAAACAGGGGG
                                                                                                                                                                                                                                                                                                                                             GACAGGTGCTGACACTTGGTCGAAATTTAATAATTTCGTAGAGAAATGACGTTGGCGGT
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'product= "parasporal body-associated protein"
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224. .4258
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                                                                                                                                               693 AGAGCTTATT----
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29-MAY-2003
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(first entry)

12-APR-2002; 2002US-00120544.

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Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;
                                                                                         ADR89411 standard; cDNA; 1986 BP.
                                                                                                                                                                                                        18-NOV-2004
                                                                                                                                                ADR89411;
                                  RESULT 14
                                                               ADR89411
                                                                                                                      This invention relates to a novel isolated polynucleotide and the encoded protein which has a larvae growth inhibiting or insecticidal effect on a Scarabaedide insect. The invention may be useful for the development of compounds with an insecticide activity. The polypeptide encoded by the gainst Scarabaedide insects such as larval growth inhibitor or insecticide compounds with an insecticide activity. The polypeptide encoded by the polymucleotide is useful as a larval growth inhibitor or insecticide composed to turf (for example golf courses), agricultural crops (for example sweet potato or peanuts), or trees. Larvae of Scarabaeidae concessed such as Anomala cuprea, Blitopertha orientalis and Popillia as the larvae are buried in the ground large amounts of pssticides, but as the larvae are buried in the ground large amounts of pssticides, but as the larvae are buried in the ground large amounts of pssticides, but as the larvae are buried in the ground large amounts of pssticides, but be used and there is a need for safer control methods. A polypeptide from Pannibacillus popillae supp. melolonthae HI has a controlling effect on provides new polypeptide have controlling effects on Anomala cuprea, Blitopertha orientalis and Popillia japonica. The invention provides new polypeptides obtained by screening Psannbacillus popillae expression libraries using antisera obtained by immunizing animals with extracts of Psenibacillus popillae species from infected Scarabaeidae controllaries. The new polypeptides are unrelated to the previously identified in the library screening against Anomala cuprae alavae showed an inhibitory effect on the larvae. The present agequence is that of a gene of the popises. The parasporal body region of Psenibacillus
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                                                                                                                                                                                                                                                                          New isolated polynucleotide encoding a protein having a larvae growth inhibiting or insecticidal effect on Scarabacidae insects, useful as controlling agent or insecticide against Scarabacidae insects such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 ATAATTACAATCGCCAACAAAGGAACTCCGCAACGTATGCAAATCATTGTACAACTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGGTGCTGACTTGGTCGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       896 CTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 ATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                   Kimura M;
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                                                                                                                 Наведама М, Ећага G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Claim 28; SEQ ID NO 19; 53pp; English.
                                                                                                              Aoyagi M,
                                                    (DNIN ) DAINIPPON INK & CHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.9
Best Local Similarity 58.0
Matches 203; Conservative
                                                                                                           Yokoyama T,
                                                                                                                                                                                            WPI; 2005-563092/57.
P-PSDB; AEB90831.
                                                                                                                                                                                                                                                                                                                                                                 Anomala cuprea
                                                                                                                                     Nishihashi H;
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                                                                                                              Tanaka M,
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셤 δ 셤 ò 요 ò g ઠે g ઠે

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This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The mucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The mucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin presence of delta-endotoxin or delta-endotoxin or presence of delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin o
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                                                                                                                      ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pesticide; resistance;
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/product= "Alternative AXMI-009 #2"
AXMI-009 alternative start site coding sequence #2.
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1. .1986
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782030.
19-FEB-2004; 2004US-00782030.
19-FEB-2004; 2004US-00782030.
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                                                                                                                                                                                                                                                                                                            pesticidal activity.
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DB 13; Length 1986;

4.8%; Score 99.6;

acide sts or

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This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, generating altered or improved delta-endotoxin or delta-endotoxin associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or delta-endotoxin or del
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                                                         isolated delta-endotoxin and delta-endotoxin-associated nucleic aci polypeptides, useful for killing lepidopteran or coleopteran pests producing organisms with pesticide resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 2016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99.6; DB 13;
Pred. No. 1.5e-12;
0; Mismatches 119;
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ne : 777.097 secs
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                                                                                                                                          21; 178pp; English
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  WPI; 2004-635574/61.
P-PSDB; ADR89410.
                                                                                                                                          SEQ ID NO
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                                                                                                                                          Claim 1;
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                                                                                                                                                                                   679 GATCATTGTATAACATTCTATAACCAGGGTTTAAATCAATTTAATC-----GCTCAAAT 732
                                                                                                                                                                                                                                                                GCTCAAGATTGGGTGAGCTTTAATAGGTTTGGTACAGATATGACATTAACAGTATTAGAT 792
                                                                                                                                                                                                                                                                                                        877 ATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAG 936
                                                                                                                                                                                                                                                                                                                                                                                         TTGACTAGGGAAATTTATACAGATGCAGTGGGATATTCATCGGGAACTTATAGTTGGTTA 996
                                                         GGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACC
                                                                                                                                                                                                                           GCTGACACTTGGTCGAAATTTAATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGAT
                                                                                                                                          757 AATTATTGTTTATATTGGTATCAGGTTAAATTCAGATAAAACAGGGGGGGACAGGT
                     Gaps
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expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
                     9
                     Indels
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Pred. No. 1.5e-12;
); Mismatches 119;
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; Sequence 2, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
    APPLICANT: Hargies, Tracy
    APPLICANT: Koziel, Michael G.
    APPLICANT: Carro. Brian
; TITLE OF INVENTION: AxM1-008, A Delta-Endotoxin Gene and
    TITLE OF INVENTION: AxM1-008, A Delta-Endotoxin Gene and
    TITLE OF INVENTION: Methods for Its Use
    TITLE NEFERENCE: 045500/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2003-02-20
; RIOR APPLICATION NUMBER: 60/448,797
; WUMBER OF SEQ ID NOS: 28
; SOFTWARE: FREISEQ for Windows Version 4.0
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Sequence 7, A
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10: /cgn2_6/ptodata/1/pubpna/USO0B_PUBCOMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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| Publication No. US20040250311A1
| GENERAL INFORMATION:
| APPLICANT: Carozzi, Nadine
| APPLICANT: Carozzi, Nadine
| APPLICANT: Carozzi, Nacholas B. APPLICANT: Cari, Brian
| APPLICANT: Cari, Brian
| TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
| TITLE OF INVENTION: Methods for Its Use
| TITLE OF INVENTION: Wethods for 128 Use
| TITLE OF INVENTION: Wethods for 128 Use
| FILE REFERENCE: 045600/274147
| CURRENT FILING DATE: 2004-02-20
| PRIOR PILING DATE: 2003-02-20
| PRIOR PILING DATE: 2003-02-20
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: FastSEQ for Windows Version 4.0
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99.6*; Score 2073; Dest Local Similarity 100.0*; Pred. No. 0; Matches 2073; Conservative 0; Mismatches
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		APPLICANT: Hargiss, Tracy APPLICANT: Hargiss, Tracy APPLICANT: Bock, Nicholael G. APPLICANT: Duck, Nicholael G. APPLICANT: Duck, Nicholael B. APPLICANT: Duck, Nicholae B. APPLICANT: Carr, Brian TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use FILE REPERENCE: 404500/274143 CURRENT APPLICATION NUMBER: 60/448,632 FILOR APPLICATION NUMBER: 60/448,632 PRIOR PILING DATE: 2003-02-20 NUMBER OF SEQ ID NOS: 23 SOFTWARE: FastSEQ for Mindows Version 4.0 SEQ ID NO 2 LENGTH: 2019 TYPE: DNA ORGANISM: Bacillus thuringiensis FEATURE: NAME/KEY: CDS NAME/KEY: CDS US-10-782-141-2.	Query Match 35.9%; Score 747.2; DB 8; Length 2019; Best Local Similarity 69.8%; Pred. No. 4e-160; Aatches 1143; Conservative 7; Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7; Qy I GTGAAAAGTGGCGATATCTAATCAAAATAAAATGAAATATGAAATATGGAATTCTGGATGGTTCCCG 60 1 GTGAAAAATATCTTATCAAAATAAAATGAAATATGAAATATGAAATATGGAAATATTCTGGTTCCCG 60 0 Qy 61 AATAACACAAATATGTCAAACAGATATCCTTTTGCAAATAATATTCCTATT 120 Qy 121 TCTTGGAATGTTCAGGGAATCTCATGGGATGAAATTTGGAAATGTTTCTATT 120 Qy 121 TCTTGGAATGTTGAGGAATCTCATGGGATGAAATTTGGGAATCAGAAACGATATTTCTTATT

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Publication No. US20040197917A1

GENERAL INFORMATION:
APPLICANT: Carcozzi, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Carci, Micholas B.
APPLICANT: Carc, Brian
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT PRLING DATE: 2004-02-20
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 4.1e-160;
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Matches 1143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 ATATACTGATTATTGCGTACATTGGTATAATCGAGGTTTCAACGAACTAAGACAACGAGG
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                                                                                                                                 Length 3471;
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                                                                                                                              8.1%; Score 168.6; DB 5; 52.5%; Pred. No. 1e-27; ative 0; Mismatches 364;
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                                                               71:
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                            Conservative
                                                                                                                                                     Similarity
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Matches 458;
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US-10-428-961-29
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US-10-099-285-71
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                      1318 AGGGTAGGGGGACCTGATTTAAATTATGATGCAGGTAATAATGGGCTAAGCAGGATGACA 1377
                                                          1270 ccgacaacacraaaracrtrccrgrargaggraaacagrrcrggg---racrcacagaca 1326
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                                                                                                                                                                                                                                                                                    TGGACACATACAAGTTTAAAACGTGAAAATATAATTGAAGCCAATCAAATTACACAAATA 1551
                                                                                                                                                                                                                                      1387 CATAGATTATCAAATGCGGCATGTGTTCAAAATGAAACCTCCAGAGTTAACGTATTTGGT
                                                                                                                                                                                              CATAGATTATCAAATGCGGCATGTTGTTATATGGAAACTCCAGAGTTAACGTATATGGT
                                                                                                          ----ATTGCACTCTAATGGTGTTAGAGGACCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/10099285
Publication No. US20030105319A1
GENERAL INFORMATION:
Micker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Ganesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILDE
COMPAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
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TELEFAX: (352) 375-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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COMPUTER READABLE FORM:
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US-10-099-285-71
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956 CAGATGCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTT 1015
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                                                   ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA
                                                                                                                                           776 ATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGGGGCAGGTGCTGACACTTGGTCGAAAT
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                                                                                                                                                                                                                                                                                                                     radegeagaaagriderrragcriterrarad 980
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 19, Application US/10120544A; Publication No. US20020182693A1; GENERAL INFORMATION:
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Best Local Similarity 58.0%;
Matches 203; Conservative 0
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ORGANISM: Bacillus popilliae
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; LOCATION: (224)..(4255)
US-10-120-544A-19
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                                                          APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Glimer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Now Tooled the Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.7%; Score 160.6; DB 6; Best Local Similarity 51.9%; Pred. No. 5.7e-26; Matches 453; Conservative 0; Mismatches 369;
Sequence 29, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Bacillus thuringiensis
US-10-428-961-29
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2407
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publication No. Us20050172355A1
publication No. Us20050172355A1
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1016 TTAATGGGTTAGAGGCTAATGGAACACGGGGACCTGGTTTAGTTACTTGG 1065
                                                          1215 TTGCAGAAATAGAAAATATCGCAATTAGGGAACCAAGCAATTTTACTTGG 1264
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4.9%; Score 102.4; DB 10; Length 4366;
Best Local Similarity 58.0%; Pred. No. 1.5e-12;
Matches 203; Conservative 0; Mismatches 141; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus popilliae
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; LOCATION: (224)..(4255)
US-11-091-654-19
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Sequence 1, Application US/10614524; Publication No. US20040016020A1; GENERAL INFORMATION:

RESULT 11 US-10-614-524-1

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publication No. US20030237111A1

Sequence 37, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Climer, Amy J.

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE FEFERENCE: MECO201-1.

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTHARE: PATENTION NUMBER: 60/153,995

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 37

LENGTH: 4173
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APPLICANT: Mathieu, Eva
APPLICANT: Wathieu, Eva
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
FILE REFERENCE: NEWBISUS2
CURRENT FILING DATE: 2003-07-08
FRIOR FILING DATE: 2003-07-08
FRIOR FILING DATE: 2000-12-19
FRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 TTACTATGAGCGATTAAAATGCAAAAGGGCAGAGTATACCAATTATTGTTTATAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 95.6; DB 7; Length 3687; 62.7%; Pred. No. 5e-11; cive 0; Mismatches 94; Indels 6
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5e-11;
94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Bacillus thuringiensis
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Boets, Annemie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATORE.
NAME/KEY: CDS
'^^ATION: (1)..(3687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3687
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US-10-428-961-37
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APPLICANT:
APPLICANT:
APPLICANT:
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1085 AAATCATTGTACCACTTGGTATCAGACGGGTTTACA-----AAGATTGCAAGGCACTAC 1138
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         CAATTAITGITTATAITGGTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGG 815
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APPLICANT: TANKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Maritchi
APPLICANT: HASEGAMA, Makoto
APPLICANT: HASEGAMA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masabaru
APPLICANT: NISHIHASHI, Hideji
ITILE OF INVENTION: POYPECTICHA effect on scarabaeidae insects and
ITILE OF INVENTION: poynucleotide encoding the same
ITILE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT PILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN UNIVER: 2201-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN UNIVER: 2201-07-04
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                                                                                                  TGCTGACACTTGGTCGAAATTTAATAATTTCGTAGAAAATGACGTTGGCGGTATTGGA
                                                                                                                                                                                        TATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGA
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Best Local Similarity 62.0%
Matches 170; Conservative
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; LOCATION: (282)..(4229)
US-11-091-654-3
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LENGTH: 4359
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                                                                                                                                                                                                                                                                                                                                                                                                                                         837 TAATAAATTICGTAGAGAAATGACGTIGGCGGTATTGGATATTATCGCTATATTICCAAC 896
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APPLICANT: YOKOYAMA, TOMOKO

APPLICANT: AOYAGT, Moriichi

APPLICANT: AOYAGT, Moriichi

APPLICANT: AOYAGT, Moriichi

APPLICANT: HASEGAWA, Makoto

APPLICANT: HASEGAWA, Hakei

APPLICANT: KIMMAS, Masaharu

APPLICANT: KIMMAS, Masaharu

APPLICANT: NISHIHASHI, Hideiji

TITLE OF INVENITON: Polypeptide having larvae growth inhibiting or

TITLE OF INVENITON: poynucleotide encoding the same

TITLE OF INVENITON: poynucleotide encoding the same

FILE REFERENCE: 0P1335

CURRENT APPLICATION NUMBER: US/10/120,544A

CURRENT PILING DATE: 2001-04-13

PRIOR PLLING DATE: 2001-04-13

PRIOR PLLING DATE: 2001-04-13

PRIOR PLLING DATE: 2001-04-13

PRIOR PLLING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 3

LENGTH: A159
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62.7%; Pred. No. 5.3e-11;
tive 0; Mismatches 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10120544A Publication No. US20020182693A1 GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus popilliae
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Best Local Similarity 62.77
Matches 168; Conservative
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Best Local Similarity 62.0
Matches 170; Conservative
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; LOCATION: (282)..(4229)
US-10-120-544A-3
                                                                                        ; LOCATION: (1)..(3687)
US-10-428-961-37
                                                                NAME/KEY: CDS
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Sequence 5, Application US/10428961
Sequence 5, Application US/10428961
Sequence 5, Application No. US2030237111A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringienais Delta-Endotoxin
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringienais Delta-Endotoxin
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringienais Of Use (Amended)
FILE REFERENCE: MECO201-1
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1
FILE OF INVENTION: POlynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1
FILE OF INVENTION NUMBER: 09/661,322
FRIOR APPLICATION NUMBER: 09/61,322
FRIOR APPLICATION NUMBER: 60/153,995
FRIOR APPLICATION NUMBER: 60/153,995
FRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 1959
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4.5%; Score 94.4; DB 6; Length 1959;
Best Local Similarity 62.2%; Pred. No. 7.1e-11;
Matches 168; Conservative 0; Mismatches 96; Indels 6
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CRGANISM: Bacillus thuringiensis
US-10-428-961-5
RESULT 15
US-10-428-961-5
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836 TTAATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAA 895
                     Sequence 19, Application US/11091643

Sequence 19, Application US/11091643

Beneral INFORMATION:

APPLICANT: TANAKA, Masao

APPLICANT: TOYCYANA, Tomoko

APPLICANT: TOYCANA, Tomoko

APPLICANT: AVCAGI, Moriichi

APPLICANT: HASEGAWA, Makoto

APPLICANT: BIARA, Gaku

APPLICANT: BIARA, Gaku

APPLICANT: BIARA, Gaku

APPLICANT: BIARA, Gaku

ITILE OF INVENTION: POLYPEPLICA = encoding the same

TITLE OF INVENTION: poynucleotide encoding the same

TITLE OF INVENTION: poynucleotide encoding the same

TITLE OF INVENTION WABER: US/11/091,643

CURRENT PILING DATE: 2005-03-29

PRIOR APPLICATION NUMBER: UP 2001-115754

PRIOR PILING DATE: 2001-04-13

PRIOR PILING DATE: 2001-07-04

SEQUENCE: PARCETING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SOPTWARE: PATENTIN Ver: 2.0

SEQUENCE: AND ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESS
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US-11-058-727-49
US-11-058-727-69
US-11-058-727-69
US-11-058-727-69
US-11-058-727-75
US-11-108-389-21
US-11-108-389-21
US-11-108-389-21
US-11-108-389-23
US-11-108-389-67
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US-11-058-727-47
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ORGANISM: Bacillus popilliae
            ; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-643-19
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Copyright (c) 1993 - 2005 Compugen Ltd.
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APPLICANT: HASCAMA, MAKOTO
APPLICANT: HASCAMA, MAKOTO
APPLICANT: HASCAMA, MAKOTO
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
APPLICANT: NISHIHASHI, Hideji
ITILE OF INVENITION: POLYPEPTICAL Effect on scarabacidae insects and
ITILE OF INVENITION: poynuclectide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,643
CURRENT APPLICATION NUMBER: US 2001-115754
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR PLING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR PLING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VET. 2.0
  TANAKA, Masao
YOKOYAMA, Tomoko
AOYAGI, Moriichi
HASEGAWA, Makoto
EHARA, Gaku
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; LOCATION: (282)..(4229)
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1095 ATTATGATGTTCGTAGTTATCCAATACAGTTACGGGGAGAGCTTACGAGAGGAATTTATA 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     882 ATAATCGATTTAGAAGAAATAACGTTAATAGTATTGGATATTTGTGCATTGTTTTCAA
                                                                 716 ATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGT
                                                                                                                                                            956 CAGATGCAGTGGGGATATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                956 CAGATGCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGAATTGGCCTAATACTT
                                                                                                                                                                                                                                                        1016 TTAATGGGTTAGAGGCTAATGGAACACGGGGACCTGGTTTAGTTACTTGG 1065
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/11070575;
Publication No. US20050271642A1
GENERAL INFORMATION:
APPLICANT: AARAO, Shin-ichiro
APPLICANT: BANDO, Hisanori
TITLE OF INVENTION: RECOMBINANT ORGANISMS PRODUCING INSECT
TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
FILE REFERENCE: 595622000300
CURRENT APPLICATION NUMBER: US/11/070,575
CURRENT FILING DATE: 2005-03-01
PRIOR APPLICATION NUMBER: US 60/549,094
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FABLEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 201; Conserv
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US-11-091-643-3
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Matches
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1085 AAATCATTGTACCACTTGGTATCAGACGGGTTTACA----AAGATTGCAAGGCACTAC 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 TGCTAGCAGTTGGCTCTCTTATCATAGATTTAGAAGAAAATGACACTAACAGTATTGGA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1199 TATTTGCGCATTATTTCAAATTATGATGCCCGTAGTTACCCACTGGAGGTAAGGGGAGA 1258
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Sequence 5, Application US/11091643

Publication No. US20050246789A1

GENERAL INFORMATION:

APPLICANT: YOKOYAMA, TOMOKO

APPLICANT: ADVAGT, MOTICIN

APPLICANT: ADVAGT, MOTICIN

APPLICANT: HASEGAWA, MAKOTO

APPLICANT: HASEGAWA, MAKOTO

APPLICANT: KIMUAT, MASABHATU

APPLICANT: KIMUAT, MASABHATU

APPLICANT: KIMUAT, MASABHATU

APPLICANT: NISHIHASHI, Hideji

TITLE OF INVENTION: POLYPEPEIGH having larvae growth inhibiting or

TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and

TITLE OF INVENTION: popuncleotide encoding the same

FILE REPERENCE: OP1335

CURRENT FILING DATE: 2005-03-29

FRIOR APPLICATION NUMBER: JF 2001-115754

FRIOR FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                          756 CAATTATTGTTTATATTGGTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           816 TGCTGACACTTGGTCGAAATTTAATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGA
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                                                                                                                                                                         696 TGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATAC
                                                                                  Gaps
                                                                                  9
Query Match
4.6%; Score 95.2; DB 9; Length 4
Best Local Similarity 62.0%; Pred. No. 1.2e-12;
Matches 170; Conservative 0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTACGAGAGAATTTATACGGATCCAGTAGCA 1292
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Sequence 3, Application US/11091643 Publication No. US20050246789A1 GENERAL INFORMATION:

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714 TGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTG 773
                                                                                                                                                                                                                                                                                                                                                                              615 GTATGAAACTGGTTTAGCAAAATTAAAA-----GGCACGAGCGCTAAACAATGGGTTGA 668
                                                                                                                                                                                                                                                                                  555 TAACTATTATGATGGCCCAAATGAACTTACTGCAGAATATTCTGATCACTGTGTAAAGTG 614
                                                                                                                                                                                                                                                                                                                                      774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGGTGCTGACATTGGTCGAA 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729 AAATTATGACACGCACGTACCCAATGGAAACGAAAGCACAACTAACAAGGAAGTATA 788
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TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPERENCE: 35110/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-05
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                                                                                                                                Score 87.8; DB 7; Length 1:
Pred. No. 4.4e-11;
0; Mismatches 112; Indels
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4.2%; Score 87.8; DB 7;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bacillus thuringiensis (truncated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-11-108-389-15
Sequence 15, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albert L. Lu
Billy Fred McCutchen
James K. Presnail
James F.H. Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
                                                                                                                                  Query Match
Best Local Similarity 59.2%;
Matches 171; Conservative
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                                 COCATION: (0)...(0)
COTHER INFORMATION: 49PVD
US-11-058-727-15
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LOCATION: (10)...(1860)
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LOCATION: (0)...(0)
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 AGTIATGATTATCGTAGTTACCCAATGGAGCTAAGGGGAGAGCTTACGAGAGAAATTTAT 999
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: James W. Kahn
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: Gac-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 3574809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
                                                                                                                                                                                                                                                                                                                                    Length 4188;
                                                                                                                                                                                                                                                                                                                            Query Match 4.4%; Score 91.4; DB 9; Length 4: Best Local Similarity 61.1%; Pred. No. 8.7e-12; Matches 168; Conservative 0; Mismatches 101; Indels
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PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 4188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Plannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
                                                                                                                                               TYPE: DNA ORGANISM: Bacillus popilliae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
FEATURE:
                                                                                                                                                                                              FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(4158)

US-11-091-643-5
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672 CTATAACCAATTCCGTAGAGAAATGACACTGGCGGTTTTAGATGTTGTTGCATTATTCCC 731
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834 ATTTAATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTCC
                                                                                                                                 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA
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                                                                                                                                                                                                                                                              TACAGATGCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGAAT 1002
                                                                                                                                                                                                                                                                                                          | APPLICANT: Abad
| APPLICANT: Ronald D. Flannagan
| APPLICANT: Ronald D. Flannagan
| APPLICANT: Rafael Herrmann
| APPLICANT: Theodore W. Kahn
| APPLICANT: Theodore W. Kahn
| APPLICANT: Theodore W. Kahn
| APPLICANT: James F. Presnail
| APPLICANT: James F. Wong
| APPLICANT: James F. Wong
| APPLICANT: Gao-Guo Yu
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| APPLICANT: Activity
| FILLE REFERENCE: 35718/291049
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TILLE OF INVENTION: Genes Encoding Proteins With Pesticidal
| TILLE OF INVENTION: UNMER: 60/491,786
| PRIOR APPLICATION NUMBER: 60/460,787
| PRIOR FILING DATE: 2003-04-04
| PRIOR FILING DATE: 2003-04-04
| PRIOR FILING DATE: 2003-04-04
| PRIOR FILING DATE: 2003-04-04
| PRIOR FILING DATE: 2003-04-04
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ORGANISM: Bacillus thuringiensis (mutated)
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Publication No. US20050261188A1
GENERAL INFORMATION:
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; OTHER INFORMATION: NGSR.N49PVD
US-11-108-389-19
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Matches 171; Conservative
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US-11-108-389-19
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555 raacrarrargarcgrcaargaaacrracrgcagaararrcrgarcacrgrgraaagrg 614
                                                                                                                          774 GTATCAGGTAGATTAAATCAGATAAAACAGGGGGGGGACAGGTGCTGACACTTGGTCGAA 833
                                                                                                                                                                                          615 GTATGAAACTGGTTTAGCAAAATTAAAA-----GGCACGAGCGCTAAACAATGGGTTGA 668
                                                                                                                                                                                                                                                           834 ATTIAATAAATTICGTAGAAATGACGTIGGCGGTATIGGATATTAICGCTATATTICC 893
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TITLE OF INVENTION: Activity
FILE REPRENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
FRIOR PEPLICATION NUMBER: 60/391,786
FRIOR FILING DATE: 2002-06-05
FRIOR RELING DATE: 2003-04-04
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 10/606,320
FRIOR APPLICATION NUMBER: 10/606,320
FRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 19
IENGTH: 1863
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4.2%; Score 87.8; DB 7; Length 1863;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6
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ORGANISM: Bacillus thuringiensis (mutated)
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Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
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OTHER INFORMATION: NGSR.N49PVD
US-11-058-727-19
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4.2%; Score 87.8; DB 7; Length 2010;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6
                                                                                                                                                                                                                             APPLICANT: Andre R. Abad
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Hermann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Ally Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
APPLICANT: Albert D. Lu
APPLICANT: Activity
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CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-04-04
PRIOR PLING DATE: 2003-06-25
PRIOR PLING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                Sequence 11, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
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; LOCATION: (1)...(2010)
; FRATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-058-727-11
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LENGTH: 2010
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RESULT 10 US-11-108-389-11

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774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGGACAGGTGCTGACATTGGTCGAA 833
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Length 2010;
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59.2%; Pred. No. 4.5e-11;
tive 0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus thuringiensis (truncated)
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Sequence'57, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
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Matches 171, Conservative
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; NAME/KEY: CDS
; LOCATION: (1) ... (2019)
US-11-058-727-59
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            APPLICANT: James F. Presnail
APPLICANT: James F. Presnail
APPLICANT: James F. Wong
APPLICANT: James F. Wong
APPLICANT: Genes F. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPRENCE: 35718/2897809
CURRENT APPLICATION NUMBER: 06/391,786
PRIOR PILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-06-04-04
PRIOR FILING DATE: 2003-06-04-04
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 2019
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APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: Ganes E. H. Wong
APPLICANT: Ganes Encoding Proteins With Pesticidal
TILLE OF INVENTION: Activity
FILE REPERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT PLING DATE: 2005-02-15
FRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
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4.2%; Score 87.8; DB 7;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112;
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ORGANISM: Bacillus thuringiensis (mutated)
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Publication No. US20050261483A1
GENERAL INFORMATION:
Billy Fred McCutchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-57
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US-11-058-727-59
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714 TGATTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATG 773
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US-21-058-72-89

Sequence 89, Application US/11058727

Publication No. US20050261483A1

SEGNERAL INFORMATION:
APPLICANT: Romald D. Flannagan
APPLICANT: Romald D. Flannagan
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
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APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
BRIOR PILING DATE: 2005-06-25
BRIOR APPLICATION NUMBER: 60/391, 786
BRIOR APPLICATION NUMBER: 10/606, 787
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICATION NUMBER: 10/606, 320
BRIOR APPLICANT: James FastSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTHARE: Z019
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4.2%; Score 87.8; DB 7; Length 2:
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Bacillus thuringiensis (mutated)
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ORGANISM: Bacillus thuringiensis (mutated)
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FRASERQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 2019
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813 CTATAACCAATTCCGTAGAGAATGACACTGGCGGTTTTAGATGTTGTTGCATTATTCCC 872
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        759 GTATGAAACTGGTTTAGCAAAATTAAAA-----GGCACGAGGGGCTAAACAATGGGTTGA 812
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APPLICANT: Andre R. Abad

APPLICANT: Ander R. Abad

APPLICANT: Rafael Herrmann

APPLICANT: Rafael Herrmann

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: James K. Presnail

APPLICANT: James K. Presnail

APPLICANT: Cac-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/291049

FILE REFERENCE: 35718/291049

FILE REPAIRENT APPLICATION NUMBER: 60/460, 787

PRIOR APPLICATION NUMBER: 10/606, 320

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: PastSEQ for Windows Version 4.0

SED ID NO 57

LENGTH: 2019
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4.2%; Score 87.8; DB 7; 1
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112;
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ORGANISM: Bacillus thuringiensis (mutated)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 57, Application US/11108389; Publication No. US20050261188A1; GENERAL INFORMATION:
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US-11-108-389-57
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GENERAL INFORMATION:

APPLICANT: Rafael Hermann

APPLICANT: Rafael Hermann

APPLICANT: Rafael Hermann

APPLICANT: Rafael Hermann

APPLICANT: Albert L. Lu

APPLICANT: James K. Presnail

APPLICANT: James F. H. Wong

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Activity

FILE REFERENCE: 35718/287809

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/287809

FILE REFERENCE: 35718/287809

FILE REFERENCE: 35718/287809

FILE REPRENCE: 35718/287809

FILE REPRING DATE: 2005-02-15

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEC ID NOS: 134

"ENGTH: 2019

"TENGTH: 2019
                                                        Length 2019;
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Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels
                                                Score 87.8; DB 7; Length 2
Pred. No. 4.5e-11;
0; Mismatches 112; Indels
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Publication No. US20050261483A1
GENERAL INFORMATION:
                                                   59.28;
                                                Query Match
Best Local Similarity 59.2
Matches 171; Conservative
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US-11-058-727-91
US-11-058-727-89
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933 TACAGATCCACTGGGCGCGGTAAACGTGTCTTCAATTGGTTCCTGGTAT 981

Search completed: December 20, 2005, 04:58:17 Job time : 137.839 secs

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Sequence
Sequence
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APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STREET: 3054 Cornwallis Road
CITY: USA
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
US-08-532-547-4
US-08-379-6658-4
US-09-019-809-4
US-09-171-177-4
US-09-100-709-3
US-08-170-709-3
US-08-170-709-3
US-08-170-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1779-046-3
US-08-1778-600-1
US-08-377-660-1
US-08-315-468-3
US-10-089-678-3
US-10-089-678-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/09001982; Patent No. 6204246; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEG ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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NAME/KEY:
LOCATION:
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  equence 5, Appl Sequence 5, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 62
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15559.937 Million cell updates/sec
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                                                                                                                                                                    December 19, 2005, 13:41:30 ; Search time 237.847 Seconds
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Sequence 71,
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Sequence 11,
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/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/cgn2 6/ptodata/1/ina/H_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCOMB.seq:*
/cgn2 6/ptodata/1/ina/RE_COMB.seq:*
/cgn2 6/ptodata/1/ina/RE_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-099-285A-71
US-09-668-650-11
US-09-661-322A-29
US-09-661-322A-29
US-09-661-322A-5
US-08-641-32A-5
US-08-61-32A-62
US-08-61-32A-62
US-08-51-547-2
US-08-51-547-2
US-08-51-547-2
US-08-51-547-2
US-08-179-656B-2
US-08-179-656B-2
US-08-179-656B-2
US-08-179-656B-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2082
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Match Length DB
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Perfect score:
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52.5%; Pred. No. 1.9e-30;
tive 0; Mismatches 364; Indels 51;
                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                          ADDRESSEE: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/001,982
FILING DATE: «Unknown»
APPLICATION NUMBER: US/09/001,982
APPLICATION NUMBER: US/09/001,982
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..3468
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3468 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE
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Matches 458; Conservative
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                                                                                                                                                                       156 AATTTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTATAGAGTTTGTGAT 215
                                                                                                                                                                                                                        153 AATAGGGGATGCAGAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTATCAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                        333 TTTACGGGTAAGTCAGAGTGTTTTAAATGATGGGATTGCAGATTTTAATGGTTCTGTACT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 TAAAGCACAATGGTTCCCATTTTTGAGTGCAGAGAATGTAAGATCGGAATTAATATCACC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 AGÁGCTTATT-----GAÁCT 707
                                                                                                                                                                                                                                                                              AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 AAATTATAGAGAGTATTATCTTTGTTTGGGGGCTTGGCTTAAAGACGGTAAACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 TGCTGAAGAACTCCGTACTCGTTTTAGAATCGCCGACTCAGAATTTGATAGAATTTTAAC
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                                                                                                                51;
                                                            Length 3468;
                                                                                                                IndelB
                                                         Score 168.6; DB 3;
Pred. No. 1.9e-30;
0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990 ITGGTTACGGAATTGGCCTAATACTTTTAATGG 1022
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; Sequence 9, Application US/09668650
; Patent No. 6780408
; GENERAL INFORMATION:
; APPLICANT: BOBCh, Hendrick J.
                                                      Wuery Match
Best Local Similarity 52.5%;
Matches 458; Conservative
  US-09-001-982-9
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153 AATAGGCGATGCAGAAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTCTTTATCAC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 TAAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCAGATTTTGACGGTAAATTGAA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTACCCAATAGAAACAGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 3471;
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               NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
ATTORNEY/AGENT INFORMATION:
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US-09-002-285-71
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                                                                                                                                                    TAAAGCACAATGGTTCCCATTTTGAGTGCAGAGAATGTAAGATCGGAATTAATATCACC
                                                                                                                                                                                                                                                                                                                         690 TAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA
                                                                                                                                                                                                                                                                                                                                                                               -----GAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768 CACTAĞIĞCTACAĞCTIĞĞITAĞAATITICATAĞATATÇĞIAĞAĞAĞAĞAĞATĞAÇATIĞATĞĞI
                                                                  CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAATGCCCAAATATTATTA
                                                                                                                       ACCTACTTTTGCACAAGCTGCAAATGTGCAGTTATTACTATTAAGGGATGCAGTTCAATA
                                                                                                                                                                                                                                                                         633 TGGCACTAATTGGGGGCTATACAATGCTACACCTTTTATAAATTATCAAAACTAGT
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                     AGATTTCAATGAAATTCTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Walz, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Tockhoff, Brian
APPLICANT: Tockhoff, Brian
APPLICANT: Tockhoff, Brian
APPLICANT: Wuller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990 TTGGTTACGGAATTGGCCTAATACTTTAATGG 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
CTTE: Florida
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
                                                                                                                                                                                                                                                                                                                                                                            693 AGAGCTTATT----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                             TCAAAAGACAAATAATTCTGATATCGGACAATTAGTTTATTATTTAAACTTTCAGAAAG
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Narce, Carol
Narce, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGTTACGGAATTGGCCTAATACTTTTAATGG 1022
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Patent No. 6752992
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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888 TITICAGITGAGITAGGGICAITTATATACAGAICCCAATTGGITTTGIACAICGIAGIAGIAGT
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Sequence 71, Application US/09589477

Sequence 71, Application US/09589477

Fatent No. 65700505

APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Watck, Carol
APPLICANT: Watz, Kenneth E.
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
8.1%; Score 168.6; DB 3;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...sainst Pee ...sainst Pee Saliwanchik STREET: 2421 N.W. 418t Street, Suite A-1 STATE: Florida COUNTRY: USA
                                                                                                            990 TIGGITACGGAATIGGCCTAATACTTTAATGG 1022
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PROBLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: Ma-701C1C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (352) 375-8800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-589-477-71
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       ------GAACT 707
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                                                                                                      708 ATATACTGATTATTGCGTACATTGGTATAATCGAGGTTTCAACGAACTAAGACAACGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/001,982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FPB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09001982;
Patent No. 6204346;
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15;
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6204246artis Corpc
     693 AGAGCTTATT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3726 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..3726
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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US-09-001-982-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 AGATITCAATGAAATICTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTATT 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rescactaatresesectatacaarscracaccrrrraraaarrarcaarcaacrast 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 crtaracadeaactaritaacadecrecaaraderecaaraacaareceaarreceare 452
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                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/866,615
FILING DATE: 1-UL-1997
APPLICATION NUMBER: US 08/674,002
ATTORNEY/AGENT: I-UL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <UNKnown>
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (352) 372-5800 INFORMATION: FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3471 base pairs
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STRANDEDNESS: single
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153 AATAGGCGATGCAGCAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTATCAC 212
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                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGIGSTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 168.6; DB 3;
52.5%; Pred. No. 1.9e-30;
ative 0; Mismatches 364;
  ADDRESSEE: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: UNKNOWN:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: UNKNOWN:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-196
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..3726
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                            ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3726 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO: 11:
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STRANDEDNESS: singl
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Matches 458; Conservative
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                                                                              153 AATAGGCGATGCAGAAAGAAGCAGTATCTATTGGGACAACCATAGTCTCTTTATCAC 212
                                                                                                                      216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT 269
                                                                                                                                                                                                                                  273 AGGTACTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATTATTATTATTATA 332
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Mismatches 364;
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Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09668650
Patent No. 6780408
GENERAL INFORMATION:
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Conservative
Matches 458;
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US-09-668-650-11
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Gaps

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APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Bonovan, William P.
APPLICANT: Rupar, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo FILE REFERENCE: MECO201
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                                               390 AAATTATAGAGAGTATTATCTTTATCTTGGGGCTTGGCTTAAAGACGGTAAACACCACT 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09661322A Patent No. 6593293 GENERAL INFORMATION:
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; LOCATION: (1)..(3687)
US-09-661-322A-37
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APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, William P.
APPLICANT: Bonovan, William P.
APPLICANT: Glimer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MCCO201
CURRENT APPLICATION NUMBER: 12/09/661,322A
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 2407
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TAAAGCACAATGGTTCCCATTTTTGAGTGCAGAGAATGTAAGATCGGAATTAATATCACC
                                                                                                            690 TAACAGTGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA
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Patent No. 6593293
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; ORGANISM: Bacillus thuringiensis
US-09-661-322A-29
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US-09-661-322A-29
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APPLICANT: Bayne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cummon, Raymond J.C.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
APPLICANT: Stelman, Steve
APPLICANT: Stelman, Steve
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: S. 10
CORRESPONDENCE ADDRESS: 10
ADDRESSEE: David R. Saliwanchik
SIRBET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704
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ZIE: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%; Score 93.4; DB 2;
62.1%; Pred. No. 1.5e-12;
iive 0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UUNE-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION WUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
                                                           Sequence 7, Application US/08448170
Patent No. 5723758
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3684 base pairs
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Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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           RESULT 11
US-08-448-170-7
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Glimer, Amy J.
APPLICANT: Glimer, Amy J.
APPLICANT: Glimer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
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4.5%; Score 94.4; DB 3; Length 1959;
Best Local Similarity 62.2%; Pred. No. 7.5e-13;
Matches 168; Conservative 0; Mismatches 96; Indels 6
           Length 4173;
                                                              Indels
                                                                 94;
        DB 3;
     Score 95.6; DB 3,
Pred. No. 4.6e-13,
0; Mismatches 94
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Patent No. 6593293
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4.6%;
  Query Match
Best Local Similarity 62.73
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu Chih-Rei
APPLICANT: Chu Chih-Rei
APPLICANT: Glamer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin ComportITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT FILLING DATE: 2000-09-13
NUMBER OF SEC ID NOS: 63
SOFTWARE: Patentin version 3.0
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759 TAATCAATTCCGTAGAGACTTAACGCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAG 818
                                                                                                                                                              TTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATAC 956
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4.5%; Score 93.4; DB 3;
Best Local Similarity 62.1%; Pred. No. 1.5e-12;
Matches 167; Conservative 0; Mismatches 96;
                                                                                                                                                                                                                                                                                           AGATCCAATTGGGAGAACAAATGCACCTT 907
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 62, Application US/09661322A
Patent No. 6593293
GENERAL INFORMATION:
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APPLICANT: LAMBERT, BART; APPLICANT: VANSENS, STEFAN APPLICANT: VAN AUDENHOVE, KATRIEN APPLICANT: PEFEROEN, MARNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMBERT, BART
JANSENS, STEFAN
VAN AUDENHOVE, KATRIEN
PEFEROEN, MARNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
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US-08-532-547-2
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                                                                                                                                                                                                                                            APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.C. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIATTATGAGCGCCAAGTGGAAAAACGAGAGAATATTCTGATTATTGCGCAAGATGGTA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATT 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717 TTACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTTTATATTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 10-UNE-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION BOTA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 13-SEPT-1995
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 13-MAY-1995
CLASSIFICATION: 800
ATTOORNEY/AGENT INPORMATION:
NAMM: ASACHARIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                             879 AGATCCAATTGGGAGAACAAATGCACCTT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                   957 AGATGCAGTGGGATATTCATCGGGAACTT
                                                                                                                                                                             Sequence 5, Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3684 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Gar
STATE: F]
COUNTRY:
                                                                                                                                                         -08-961-803-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-961-803-5
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                                                             셤
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Application US/08379656B

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               999 CATCAATICCGIAGAAATGACITIIAGIGGIATIAGAIGIIGIGGGGGCIATITCCAIAI 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1059 TATGATGTACGACTTTATCCAACGGGATCAAACCCACAGGCTTACACGTGAGGTATATACA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718 TACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGTAT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885 TATTATGACCGTCAATTGGAACTAACCGCTAAGTACACTAATTACTGTGAAACTTGGTAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   778 CAGGTAGGTTTAAATCAGATAAAACAGGGGGGGGGCGGTGCTGACACTTGGTCGAAATTT 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945 AATACAGGTTTAGATCGTTTAAGA-----GGAACAATACTGAAAGTTGGTTAAGATAT 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 AATAAATTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898 TATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACA 957
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN RIE, JEROEN
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
COUNTRY: Reals Church
STREET: P.O. Box 747
CITY: Reals Church
STREET: P.O. Box 747
CITY: Reals Church
STREET: P.O. Box 747
COUNTRY: USA
ZIP: 22040-0747
COUNTRY: USA
ZIP: 22040-0747
COUNTRY: USA
ZIP: 22040-0747
COUNTRY: BW PC COMPable
COUNTRY: BW PC COMPable
COUNTRY: BW PC COMPable
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: PREADABLE FORM:
MEDIUM TYPE: Ploppy disk
COUNTRY: APPLICATION DATA:
APPLICATION NUMBER: US/08/532,547
FILING DATE: O6-DEC-196
ATTORNEY/AGENT INPORMATION:
NAME: SYENSON, LEGONARD R.
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 2121-109P
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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NAME/KEY: misc feature
LOCATION: 1..1561
OTHER INFORMATION: /note= "contains the translation
OTHER INFORMATION: initiation codon of the bTS02618A gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.5%; Score 93; DB 2; Length 1561;
Best Local Similarity 61.5%; Pred. No. 1.5e-12;
Matches 169; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1119 GATCCGATTGTATTTAATCCACCAGCTAATGTTGG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 GAIGCAGIGGGAIAIICAICGGGAACTIAIAGIIG 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: BTS02618A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   名
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RESULT 15 US-08-379-656B-2

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885 TATTATGACCGTCAATTGGAACTAACCGCTAAGTACACTAATTACTGTGAAACTTGGTAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           945 aatacaggititagatcgittaaga-----ggaacaaatacigaagtiggitaagatat 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   718 TACTATGAGCGATTAAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
GENERAL INFORMATION:
APPLICANT: Lambert Bart
APPLICANT: Janeen, Stefan
APPLICANT: Van Andenhove, Katrien
APPLICANT: Van Andenhove, Katrien
APPLICANT: Pefercen, Marnix
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falle Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
CCATION: 1..1561
OTHER INFORMATION: /note= "contains the translation;
OTHER INFORMATION: initiation codon of the bTS02618A gene"
US-08-379-656B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1561;
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTUTER: IBM PC compatible
COMPTUTER: IBM PC compatible
COMPTUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/379,656B
FILING DATE: 12-MULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EB93/01820
FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93400949.9
FILING DATE: 09-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92402358.8
FILING DATE: 27-AUG-1992
ATONNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 30,330
REFERENCE/POCKET NUMBER: 31,330
REFERENCE/POCKET NUMBER: 31,330
REFERENCE/POCKET NUMBER: 31,330
REFERENCE/POCKET NUMBER: 31,330
RELEPAK: (703) 205-8000
TELLEPAK: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus thuringiensis
STRAIN: BTS02618A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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